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(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005

L1 26021 S EGEG/SQSP

FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005

L2 4892 S L1

L3 643 S (FUSION OR CHIMER? OR CHIMAER?) (5A)PROTEIN? AND L2

L4 6 S L3 AND CAPTUR?

L5 0 S L3 AND POLYCATION?

L6 2 S L2 AND POLYCATION?

SELECT L6 RN 1-2

L7 361075 S E1-828

FILE 'REGISTRY' ENTERED AT 09:32:39 ON 02 AUG 2005

L8 0 S (AG){3-6}EG{14-36}/SQSP

L9 271929 S (AG){0-8}EG{2-40}/SQSP

L10 271887 S .{2-}(AG){0-8}EG{2-40}|(AG){0-8}EG{2-40}.{2-}/SQSP

L11 271858 S SQL>=6 AND L10

FILE 'HCAPLUS' ENTERED AT 09:58:13 ON 02 AUG 2005

L12 32705 S L11

L13 10387 S L12 AND ?CATION?

FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005

L14 26011 S .{2-}(AG){0-8}(EG){2-40}|(AG){0-8}(EG){2-40}.{2-}/SQSP

L15 146 S .{2-}(AG){0-8}(PEG){2-40}|(AG){0-8}(PEG){2-40}.{2-}/SQSP

L16 26156 S L14 OR L15

FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005

L17 4920 S L16

L18 2014 S L17 AND ?CATION?

L19 15 S L18 AND CAPTUR?

L20 25 S L18 AND SOLID(3A)SUPPORT?

L21 0 S L20 AND TAIL?

L22 44 S L18 AND TAIL?

L23 1 S L18 AND ?POLYMER?(3A)TAIL?

L24 3 S L18 AND TETHER?

L25 2011 S L18 NOT L24

L26 2 S L25 AND POSITIV? AND NEGATIV?

L27 2009 S L25 NOT L26

L28 1 S L27 AND POLYLYSINE?

L29 2 S L17 AND POLYLYSINE?

FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005

L30 1 S 775512-26-0

FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005

FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005

L31 1 S 775512-27-1

L32 26011 S .{2-}(AG){0-8}(EG){2-40}^|^(AG){0-8}(EG){2-40}.{2-}|^.{2-}(AG

L33 146 S .{2-}(AG){0-8}(PEG){2-40}^|^(AG){0-8}(PEG){2-40}.{2-}|^.{2-}(

L34 26156 S L32 OR L33

FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005

L35 4920 S L34

L36 1 S L27 AND POLYARGININE

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L37      1 S L17 AND POLYARGININE
L38      1 S L17 AND POLYARGININE?
L39      2 S L27 AND ANION?(2A)BIND?
L40      4 S L27 AND CATION(2A)BIND?
L41      2 S L27 AND ?ANION?(2A) (BIND? OR BOUND?)
L42      51 S L27 AND ?CATION?(2A)BIND?
L43      0 S L27 AND ?CATION?(2A)BOUND?
L44      1 S L42 AND MATRI?
L45      50 S L42 NOT L44
L46      79 S L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR L36-L45
L47      13 S PY<2001 AND L46
          DELETE SELECT
          SELECT L47 RN 1-13
          DELETE SELECT

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FILE 'REGISTRY' ENTERED AT 12:11:11 ON 02 AUG 2005

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L48      FILE 'HCAPLUS' ENTERED AT 12:11:23 ON 02 AUG 2005
          TRA L47 1-13 RN :      4216 TERMS

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L49      FILE 'REGISTRY' ENTERED AT 12:11:25 ON 02 AUG 2005
          4216 SEA L48
L50      58 S L49 AND L16

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L51      FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005
          13 S L47 AND L50

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=> d ibib abs 151 1-13

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L51 ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER:      2003:42910 HCAPLUS
DOCUMENT NUMBER:      138:102669
TITLE:                  Engineered construction of long-wavelength variants of
                        Aequorea green fluorescent protein by computational
                        modeling from its three-dimensional crystal structure
INVENTOR(S):           Wachter, Rebekka M.; Remington, S. James
PATENT ASSIGNEE(S):    USA
SOURCE:                 U.S. Pat. Appl. Publ., 100 pp., Cont.-in-part of U. S.
                        6.077,707.
                        CODEN: USXXCO
DOCUMENT TYPE:          Patent
LANGUAGE:               English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

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PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003013149	A1	20030116	US 2000-575847	20000519
US 6593135	B2	20030715		
US 6124128	A	20000926	US 1996-706408	19960830 <--
US 6054321	A	20000425	US 1997-911825	19970815 <--
EP 1508574	A2	20050223	EP 2004-24850	19970815
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6077707	A	20000620	US 1997-974737	19971119 <--
AU 767375	B2	20031106	AU 2001-23196	20010223
CA 2408302	AA	20011129	CA 2001-2408302	20010517
WO 2001090147	A2	20011129	WO 2001-US16149	20010517
WO 2001090147	A3	20020502		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				

CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

EP 1285065 A2 20030226 EP 2001-937550 20010517

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

JP 2004502410 T2 20040129 JP 2001-586334 20010517

US 2004014128 A1 20040122 US 2003-620099 20030714

PRIORITY APPLN. INFO.: US 1996-24050P P 19960816

US 1996-706408 A1 19960830

US 1997-911825 A1 19970815

US 1997-974737 A2 19971119

AU 1997-43277 A3 19970815

EP 1997-941350 A3 19970815

US 2000-575847 A 20000519

WO 2001-US16149 W 20010517

AB Engineered fluorescent proteins, nucleic acids encoding them, and methods of use are provided. As a step in understanding the properties of green fluorescent protein (GFP) from *Aequorea victoria*, and to aid in the tailoring of GFPs with altered characteristics, the 3-dimensional structure was determined at 1.9 Å resolution of the S65T mutant. Spectral properties of Thr203 mutants in comparison to S65T are provided. In particular, the S65G/V68L/S72A/T203Y (designated yellow fluorescent protein or YFP) displays an excitation maximum at 514 nm, an emission maximum at 527 nm, extinction coefficient of 83,400 M⁻¹cm⁻¹, and quantum yield of 0.61; its absorption spectrum is a function of NaCl concentration, demonstrating its usefulness as a halide sensor. Crystallog. **identification** and description of halide binding sites indicates a relationship between **anion binding** and cavity size, a relaxation of the β-barrel conformation in response to the H148Q substitution and iodide binding, and the key residues for **anion binding** are determined by mutational anal.

L51 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:717215 HCAPLUS

DOCUMENT NUMBER: 134:176440

TITLE: **Identification** of nucleolar protein No55 as a tumour-associated autoantigen in patients with prostate cancer

AUTHOR(S): Fossa, A.; Siebert, R.; Aasheim, H.-C.; Maelandsmo, G. M.; Berner, A.; Fossa, S. D.; Paus, E.; Smeland, E. B.; Gaudernack, G.

CORPORATE SOURCE: Department of Immunology, The Norwegian Radium Hospital, Oslo, 0310, Norway

SOURCE: British Journal of Cancer (2000), 83(6), 743-749

CODEN: BJCAAI; ISSN: 0007-0920

PUBLISHER: Harcourt Publishers Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Four different genes were identified by immunoscreening of a cDNA expression library from the human prostate cancer cell line DU145 with allogeneic sera from four prostate cancer patients. A cDNA encoding the nucleolar protein No55 was further analyzed and shown to be expressed at

the mRNA level in several normal tissues, including ovaries, pancreas and prostate and in human prostate cancer cell lines PC-3, PC-3m and LNCaP. By reverse transcriptase/polymerase chain reaction, expression of No55 was several-fold higher in two out of nine prostate cancer primary tumors and two out of two metastatic lesions, compared to normal prostate tissue. Antibodies to No55 were detected in sera from seven out of 47 prostate cancer patients but not in sera from 20 healthy male controls. Sequence anal. of the No55 open reading frame from normal and tumor tissues revealed no tumor-specific mutations. The No55 gene was located to chromosome 17q21, a region reported to be partially deleted in prostate cancer. Considering the immunogenicity of the No55 protein in the tumor host, the expression profile and chromosomal localization of the corresponding gene, studies evaluating No55 as a potential antigen for immunol. studies in prostate cancer may be warranted.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:697875 HCAPLUS

DOCUMENT NUMBER: 134:290979

TITLE: Isoforms of JSAP1 scaffold protein generated through alternative splicing

AUTHOR(S): Ito, M.; Akechi, M.; Hirose, R.; Ichimura, M.; Takamatsu, N.; Xu, P.; Nakabeppu, Y.; Tadayoshi, S.; Yamamoto, K.-i.; Yoshioka, K.

CORPORATE SOURCE: School of Science, Department of Biosciences, Kitasato University, Sagamihara, Kanagawa, 228-8555, Japan

SOURCE: Gene (2000), 255(2), 229-234
CODEN: GENED6; ISSN: 0378-1119

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have identified four isoforms of c-Jun NH2-terminal kinase (JNK)/stress-activated protein kinase-associated protein 1 (JSAP1), a scaffold protein that participates in JNK mitogen-activated protein kinase cascades, termed JSAP1a, JSAP1b, JSAP1c, and JSAP1d. The previously identified JSAP1 was renamed JSAP1a to avoid confusion. Analyses of the exon-intron structure of the jsap1 gene indicated that the isoforms are generated through alternative splicing involving exons 5 and 6. The mRNA expression levels of the JSAP1 isoforms differed among the mouse tissues examined. We also investigated the region of JSAP1 responsible for its interaction with JNK, and found that the JNK-binding domain is located between aa residues 201 and 217 in JSAP1a, which is encoded by part of exon 6. As all the JSAP1 isoforms contain this binding domain, we examined the binding affinity of the JSAP1 isoforms for JNK1, JNK2, and JNK3. JSAP1c and JSAP1d, which contain a 31-aa sequence not present in JSAP1a or JSAP1b, had a lower binding affinity for the JNKs, especially JNK3. These results suggest that JSAP1c and JSAP1d may attenuate the scaffolding activity of JSAP1a and/or JSAP1b in JNK cascades, especially the JNK3 cascades.

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:627482 HCAPLUS

DOCUMENT NUMBER: 133:262900

TITLE: Sequence similarities between a novel putative G protein-coupled receptor and Na⁺/Ca²⁺ exchangers define a **cation binding** domain

AUTHOR(S): Nikkila, Heli; McMillan, D. Randy; Nunez, Brian S.; Pascoe, Leigh; Curnow, Kathleen M.; White, Perrin C.

CORPORATE SOURCE: Division of Pediatric Endocrinology, University of Texas Southwestern Medical Center, Dallas, TX, 75235-9063, USA

SOURCE: Molecular Endocrinology (2000), 14(9), 1351-1364
CODEN: MOENEN; ISSN: 0888-8809

PUBLISHER: Endocrine Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB CDNA clones encoding a novel putative G protein-coupled receptor have been characterized. The receptor is widely expressed in normal solid tissues. Consisting of 1967 amino acid residues, this receptor is one of the largest known and is therefore referred to as a very large G protein-coupled receptor, or VLGR1. It is most closely related to the secretin family of G protein-coupled receptors based on similarity of the sequences of its transmembrane segments. As demonstrated by cell surface labeling with a biotin derivative, the recombinant protein is expressed on the surface of transfected mammalian cells. Whereas several other recently described receptors in this family also have large extracellular domains, the large extracellular domain of VLGR1 has a unique structure. It has nine imperfectly repeated units that are rich in acidic residues and are spaced at intervals of approx. 120 amino acid residues. These repeats resemble the regulatory domains of Na⁺/Ca²⁺ exchangers as well as a component of an extracellular aggregation factor of marine sponges. Bacterial fusion proteins containing two or four repeats specifically bind ⁴⁵Ca in overlay expts.; binding is competed poorly by Mg²⁺ but competed well by neomycin, Al³⁺, and Gd³⁺. These results define a consensus **cation binding** motif employed in several widely divergent types of proteins. The ligand for VLGR1, its function, and the signaling pathway(s) it employs remain to be defined.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:613167 HCAPLUS

DOCUMENT NUMBER: 133:218310

TITLE: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*

AUTHOR(S): Heidelberg, John F.; Elsen, Jonathan A.; Nelson, William C.; Clayton, Rebecca A.; Gwinn, Michelle L.; Dodson, Robert J.; Haft, Daniel H.; Hickey, Erin K.; Peterson, Jeremy D.; Umayam, Lowell; Gill, Steven R.; Nelson, Karen E.; Read, Timothy D.; Tettelin, Herve; Richardson, Delwood; Ermolaeva, Maria D.; Vamathevan, Jessica; Bass, Steven; Qin, Haiying; Dragoi, Ioana; Sellers, Patrick; McDonald, Lisa; Utterback, Teresa; Fleishmann, Robert D.; Nierman, William C.; White, Owen; Salzberg, Steven L.; Smith, Hamilton O.; Colwell, Rita R.; Mekalanos, John J.; Venter, J. Craig; Fraser, Claire M.

CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA

SOURCE: Nature (London) (2000), 406(6795), 477-483
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The complete genomic sequence of the gram-neg., γ -Proteobacterium *Vibrio cholerae* El Tor N16961 was determined to be 4,033,460 bp. The genome consists of two circular chromosomes of 2,961,146 bp and 1,072,314 bp that

together encode 3885 open reading frames. The vast majority of recognizable genes for essential cell functions (such as DNA **replication**, transcription, translation, and cell-wall biosynthesis) and pathogenicity (for example, toxins, surface antigens, and adhesins) are located on the large chromosome. In contrast, the small chromosome contains a larger fraction (59%) of hypothetical genes compared with the large chromosome (42%), and also contains many more genes that appear to have origins other than the γ -Proteobacteria. The small chromosome also carries a gene **capture** system (the integron island) and host 'addiction' genes that are typically found on plasmids; thus, the small chromosome may have originally been a megaplasmid that was **captured** by an ancestral *Vibrio* species. The *V. cholerae* genomic sequence provides a starting point for understanding how a free-living, environmental organism emerged to become a significant human bacterial pathogen.

REFERENCE COUNT: 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2000:4884 HCAPLUS

DOCUMENT NUMBER: 132:163331

TITLE: env sequences of simian immunodeficiency viruses from chimpanzees in Cameroon are strongly related to those of human immunodeficiency virus group N from the same geographic area

AUTHOR(S): Corbet, Sylvie; Muller-Trutwin, Michaela C.; Versmisse, Pierre; Delarue, Severine; Ayoub, Ahidjo; Lewis, John; Brunak, Soren; Martin, Paul; Brun-Vezinet, Francoise; Simon, Francois; Barre-Sinoussi, Francoise; Maucclere, Philippe

CORPORATE SOURCE: Unite de Biologie des Retrovirus, Institut Pasteur, Paris, Fr.

SOURCE: Journal of Virology (2000), 74(1), 529-534

CODEN: JOVIAM; ISSN: 0022-538X

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Human immunodeficiency virus type 1 (HIV-1) group N from Cameroon is phylogenetically close, in env, to the simian immunodeficiency virus (SIV) cpz-gab from Gabon and SIVcpz-US of unknown geog. origin. We screened 29 wild-born Cameroonian chimpanzees and found that three (Cam3, Cam4, and Cam5) were pos. for HIV-1 by Western blotting. Mitochondrial DNA sequence anal. demonstrated that Cam3 and Cam5 belonged to Pan troglodytes troglodytes and that Cam4 belonged to P. t. vellerosus. Genetic analyses of the viruses together with serol. data demonstrated that at least one of the two P. t. troglodytes chimpanzees (Cam5) was infected in the wild, and revealed a horizontal transmission between Cam3 and Cam4. These data confirm that P. t. troglodytes is a natural host for HIV-1-related viruses. Furthermore, they show that SIVcpz can be transmitted in captivity, from one chimpanzee subspecies to another. All three SIVcpz-cam viruses clustered with HIV-1 N in env. The full Cam3 SIVcpz genome sequence showed a very close phylogenetic relationship with SIVcpz-US, a virus identified in a P. t. troglodytes chimpanzee **captured** nearly 40 yr earlier. Like SIVcpz-US, SIVcpz-cam3 was closely related to HIV-1 N in env, but not in pol, supporting the hypothesis that HIV-1 N results from a recombination event. SIVcpz from chimpanzees born in the wild in Cameroon are thus strongly related in env to HIV-1 N from Cameroon, demonstrating the geog. coincidence of these human and simian viruses and providing a further strong argument in favor of the origin of HIV-1 being in chimpanzees.

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1999:766689 HCAPLUS

DOCUMENT NUMBER: 132:133025

TITLE: **Identification** of a Novel Homolog of the Drosophila staufer Protein in the Chromosome 8q13-q21.1 Region

AUTHOR(S): Buchner, Georg; Bassi, Maria Teresa; Andolfi, Grazia; Ballabio, Andrea; Franco, Brunella

CORPORATE SOURCE: Telethon Institute of Genetics and Medicine (TIGEM), Milan, Italy

SOURCE: Genomics (1999), 62(1), 113-118

CODEN: GNMCEP; ISSN: 0888-7543

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We report the **identification** of a new transcript homologous to the Drosophila staufer protein. This transcript, named STAU2 (HGMW-approved gene symbol and name), maps to the chromosome 8q13-q21 region. The full-length STAU2 cDNA is 4058 bp and contains an open reading frame of 479 amino acids. Anal. of the predicted protein product indicated the presence of three double-stranded RNA-binding domains. Best-fit anal. revealed a 48.5% similarity to the Drosophila protein and a 59.9% similarity to the recently described mammalian homolog hStau, indicating that at least two different transcripts with homologies to the fly protein are present in mammals. (c) 1999 Academic Press.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1999:594265 HCAPLUS

DOCUMENT NUMBER: 131:320676

TITLE: mAKAP: an A-kinase anchoring protein targeted to the nuclear membrane of differentiated myocytes

AUTHOR(S): Kapiloff, Michael S.; Schillace, Robynn V.; Westphal, Ann M.; Scott, John D.

CORPORATE SOURCE: Howard Hughes Medical Institute, Vollum Institute, Portland, OR, 97201-3098, USA

SOURCE: Journal of Cell Science (1999), 112(16), 2725-2736

CODEN: JNCSAI; ISSN: 0021-9533

PUBLISHER: Company of Biologists Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The compartmentalization of second messenger-activated protein kinases contributes to the fidelity of hormone-mediated signal transduction events. For example, the cAMP-dependent protein kinase is **tethered** at specific intracellular **locations** through association with A-kinase anchoring proteins (AKAPs). The authors now report the cloning of mAKAP, an anchoring protein found predominantly in heart, skeletal muscle and brain, and whose expression is induced in neonatal ventriculocytes by treatment with hypertrophic stimuli. MAKAP is targeted to the nuclear membrane of differentiated myocytes. Anal. of mAKAP-green fluorescent protein (GFP) fusion constructs revealed that nuclear membrane targeting is conferred by two regions of the protein, between residues 772-915 and 915-1065, which contain spectrin-like repeat sequences. Heterologous expression of the mAKAP targeting sequences displaced the endogenous anchoring protein from the nuclear membrane, demonstrating that

mAKAP targeting is saturable. Collectively, these data suggest that a domain containing spectrin-like repeats mediates targeting of the anchoring protein mAKAP and the cAMP-dependent protein kinase holoenzyme to the nuclear membrane in response to differentiation signals.

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1998:460763 HCAPLUS

DOCUMENT NUMBER: 129:185689

TITLE: **Identification** of a human PTS1 receptor docking protein directly required for peroxisomal protein import

AUTHOR(S): Fransen, Marc; Terlecky, Stanley R.; Subramani, Suresh
CORPORATE SOURCE: Department of Biology, University of California at San Diego, La Jolla, CA, 92093-0322, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (1998), 95(14), 8087-8092

CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The discovery of many fatal human disorders resulting from impaired peroxisomal protein import makes the functional characterization of human peroxins critical. As part of our attempt to identify novel human genes and gene products involved in the import of peroxisomal proteins, the authors raised antisera against peroxisomal membrane proteins. One such antiserum inhibited peroxisomal protein import in semipermeabilized mammalian cells. This "import inhibiting" antiserum, ab-MF3, specifically recognized a 57-kDa protein. Immunoblot anal. of rat liver subcellular fractions demonstrated that this protein was present exclusively in peroxisomal membranes. Functional anal. revealed that this 57-kDa mol. bound the PTS1 receptor, Tcx5p, in ligand blots, suggesting it is a docking site on the peroxisomal membrane. Previous studies have identified two yeast proteins, Pex14p and Pex13p, as Pex5p-binding proteins. To facilitate the biochem. anal. of peroxisomal membrane docking proteins, the authors cloned and expressed the previously unidentified human Pex14p, as well as a human Pex13p that is 39 aa longer than previously reported. Recombinant Pex14p was specifically recognized by the "import inhibiting" ab-MF3 and bound Pex5p and the Src homol. 3 (SH3) domain of Pex13p in ligand blots. These studies demonstrate that the ab-MF3-immunoreactive, 57-kDa peroxisomal membrane protein is Pex14p. Furthermore, this peroxin interacts with Pex5p and Pex13p(SH3) and is directly required for peroxisomal protein import.

REFERENCE COUNT: 33 THERE ARE 33 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L51 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1996:424017 HCAPLUS

DOCUMENT NUMBER: 125:110877

TITLE: Association of human protein-tyrosine phosphatase κ with members of the Armadillo family

AUTHOR(S): Fuchs, Miriam; Mueller, Thomas; Lerch, Markus M.; Ullrich, Axel

CORPORATE SOURCE: Dep. Molecular Biol., Max-Planck-Inst. Biochemie, Martinsried, 82152, Germany

SOURCE: Journal of Biological Chemistry (1996), 271(28), 16712-16719
CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A human receptor-like protein-tyrosine phosphatase (PTP) was identified in the mammary carcinoma cell line SK-BR-3, which represents the human homolog of murine PTP κ and was therefore termed hPTP κ . The hPTP κ expression is dependent on cell d. and is colocalized with 2 members of the arm family of proteins, β -catenin and γ -catenin/plakoglobin, at adherens junctions. Both in vitro and in vivo binding assays demonstrated specific complex formation between endogenous hPTP κ and β - and γ -catenin/plakoglobin. In addition, evidence that suggests that β -catenin may represent a substrate for the catalytic activity of hPTP κ . The **identification** of specific **binding** partners for this receptor-like PTP provides insight into the mechanisms of its biol. action and suggests a role for hPTP κ in the regulation of processes involving cell contact and adhesion such as growth control, tumor invasion, and metastasis.

L51 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 1996:137493 HCAPLUS
 DOCUMENT NUMBER: 124:222269
 TITLE: **Identification** and characterization of a thermostable MutS homolog from Thermus aquaticus
 AUTHOR(S): Biswas, Indranil; Hsieh, Peggy
 CORPORATE SOURCE: Genetics & Biochemistry Branch, NIDDK, Bethesda, MD, 20892-1810, USA
 SOURCE: Journal of Biological Chemistry (1996), 271(9), 5040-8
 CODEN: JBCHA3; ISSN: 0021-9258
 PUBLISHER: American Society for Biochemistry and Molecular Biology
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB Recognition of mispaired or unpaired bases during DNA mismatch repair is carried out by the MutS protein family. Here, the authors describe the isolation and characterization of a thermostable MutS homolog from Thermus aquaticus YT-1. Sequencing of the mutS gene predicts an 89.3-kDa polypeptide sharing extensive amino acid sequence homol. with MutS homologs from both prokaryotes and eukaryotes. Expression of the T. aquaticus mutS gene in Escherichia coli results in a dominant mutator phenotype. Initial biochem. characterization of the thermostable MutS protein, which was purified to apparent homogeneity, reveals two thermostable activities, an ATP hydrolysis activity in which ATP is hydrolyzed to ADP and Pi and a specific DNA mismatch binding activity with affinities for heteroduplex DNAs containing either an insertion/deletion of one base or a GT mismatch. The ATPase activity exhibits a temperature optimum of approx. 80°C. Heteroduplex DNA binding by the T. aquaticus MutS protein requires Mg²⁺ and occurs over a broad temperature range from 0°C to at least 70°C. The thermostable MutS protein may be useful for further biochem. and structural studies of mismatch **binding** and for **applications** involving mutation detection.

L51 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 1995:301696 HCAPLUS
 DOCUMENT NUMBER: 122:179969
 TITLE: Nucleotide sequence and mutational analysis indicate that two Helicobacter pylori genes encode a P-type ATPase and a **cation-binding**

protein associated with copper transport
 AUTHOR(S): Ge, Zhongming; Hiratsuka, Koji; Taylor, Diane E.
 CORPORATE SOURCE: Dep. Med. Microbiol. Infectious Diseases, Univ.
 Alberta, Edmonton, AB, T6G 2H7, Can.
 SOURCE: Molecular Microbiology (1995), 15(1), 97-106
 CODEN: MOMIEE; ISSN: 0950-382X
 PUBLISHER: Blackwell
 DOCUMENT TYPE: Journal
 LANGUAGE: English
 AB A 2.7-kb fragment of Helicobacter pylori UA802 chromosomal DNA was cloned and sequenced. Three open reading frames (designated ORF1, ORF2 and ORF3, resp.) were predicted from the DNA sequence, of which ORF1 and ORF2 appeared to be located within the same operon. The deduced 611-amino-acid sequence of ORF1, a P-type ATPase (designated hpCopA), had striking homol. (29-38%) with several bacterial P-type ATPases and contained the potential functional domains conserved in P-type ATPases from various sources ranging from bacterial to human. A protein of 66 amino acids (designated hpCopP) encoded by ORF2 shared extensive sequence similarity with MerP, a periplasmic mercuric ion-transporting protein, and contains the heavy metal-binding motif. Disruption of ORF1 with a chloramphenicol-resistance cassette (CAT) rendered the H. pylori mutants more susceptible to cupric ion than their parental strains, whereas there is no significant alternation of susceptibility to Ni²⁺, Cd²⁺ and Hg²⁺ between the mutants and the parental strains. The results obtained indicate that ORF1 and ORF2 comprise a **cation**-transporting system which is associated with copper export out of the H. pylori cells.

L51 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 2005 ACS on STN
 ACCESSION NUMBER: 1993:443606 HCAPLUS
 DOCUMENT NUMBER: 119:43606
 TITLE: **Identification** and preliminary
 characterization of a protein motif related to the
 zinc finger
 AUTHOR(S): Lovering, Ruth; Hanson, Isabel M.; Borden, Katherine
 L. B.; Martin, Stephen; O'Reilly, Nicola J.; Evan,
 Gerard I.; Rahman, Dinah; Pappin, Darryl J. C.;
 Trowsdale, John; Freemont, Paul S.
 CORPORATE SOURCE: Hum. Immunogenet. Lab., Imp. Cancer Res. Fund, London,
 WC2A 3PX, UK
 SOURCE: Proceedings of the National Academy of Sciences of the
 United States of America (1993), 90(6),
 2112-16
 CODEN: PNASA6; ISSN: 0027-8424
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB A protein motif related to the zinc finger was identified which defines a newly discovered family of proteins. The motif was found in the sequence of the human RING1 gene, which is proximal to the major histocompatibility complex region on chromosome 6. The name RING finger is proposed for this motif, which is found in 27 proteins, all of which have putative DNA binding functions. A peptide corresponding to the RING1 motif was synthesized and a number of its properties, including metal and DNA binding, were examined. The RING finger motif appears to be the DNA-binding domain of this newly defined family of proteins.

=> d his full

(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

L1 FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005
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L2 FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005
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L3 643 SEA (FUSION OR CHIMER? OR CHIMAER?) (5A)PROTEIN? AND L2
L4 6 SEA L3 AND CAPTUR?
L5 0 SEA L3 AND POLYCATION?
L6 2 SEA L2 AND POLYCATION?

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L9 271929 SEA (AG){0-8}EG{2-40}/SQSP
L10 271887 SEA .{2-}(AG){0-8}EG{2-40}|(AG){0-8}EG{2-40}..{2-}/SQSP
L11 271858 SEA SQL>=6 AND L10

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32705 SEA L11
L13 10387 SEA L12 AND ?CATION?

L14 FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005
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L16 26156 SEA L14 OR L15

FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005

L17 4920 SEA L16
 L18 2014 SEA L17 AND ?CATION?
 L19 15 SEA L18 AND CAPTUR?
 L20 25 SEA L18 AND SOLID(3A)SUPPORT?
 L21 0 SEA L20 AND TAIL?
 L22 44 SEA L18 AND TAIL?
 L23 1 SEA L18 AND ?POLYMER?(3A)TAIL?
 D SCAN
 L24 3 SEA L18 AND TETHER?
 D SCAN
 L25 2011 SEA L18 NOT L24
 L26 2 SEA L25 AND POSITIV? AND NEGATIV?
 D SCAN
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 L27 2009 SEA L25 NOT L26
 L*** DEL 0 S BLOCK(A)HOMOPOLYMER? (5A)AMINO (3A)ACID
 L*** DEL 18 S BLOCK(A)POLYMER? (5A)AMINO (3A)ACID
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 L28 1 SEA L27 AND POLYLYSINE?
 D SCAN
 L29 2 SEA L17 AND POLYLYSINE?

FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005

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 D SCAN
 D SQIDE L30

FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005

D SCAN L29

FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005

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 L32 26011 SEA .{2-}(AG){0-8}(EG){2-40}^|^ (AG){0-8}(EG){2-40} .{2-}|^.{2-}(
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 L34 26156 SEA L32 OR L33

FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005

L35 4920 SEA L34
 L36 1 SEA L27 AND POLYARGININE
 L37 1 SEA L17 AND POLYARGININE
 L38 1 SEA L17 AND POLYARGININE?
 L*** DEL 624 S L27 AND BIND?
 L39 2 SEA L27 AND ANION?(2A)BIND?
 L40 4 SEA L27 AND CATION(2A)BIND?
 D SCAN L39
 D SCAN
 L*** DEL 0 S L27 AND POLYANION?(2A)BIND?
 L41 2 SEA L27 AND ?ANION?(2A) (BIND? OR BOUND?)
 D SCAN
 L42 51 SEA L27 AND ?CATION?(2A)BIND?
 L43 0 SEA L27 AND ?CATION?(2A)BOUND?
 L44 1 SEA L42 AND MATRI?
 D SCAN
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 D TI 1-2
 D TI 2-20

L46 79 SEA L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR (L36 OR L37 OR
L38 OR L39 OR L40 OR L41 OR L42 OR L43 OR L44 OR L45)
L47 13 SEA PY<2001 AND L46
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DELETE SELECT
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DELETE SELECT

FILE 'REGISTRY' ENTERED AT 12:11:11 ON 02 AUG 2005

FILE 'HCAPLUS' ENTERED AT 12:11:23 ON 02 AUG 2005
L48 TRA L47 1-13 RN : 4216 TERMS

FILE 'REGISTRY' ENTERED AT 12:11:25 ON 02 AUG 2005
L49 4216 SEA L48
L50 58 SEA L49 AND L16
L*** DEL 0 S HCAPLUS

FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005
L51 13 SEA L47 AND L50
D IBIB ABS L51 1-13

FILE HOME

FILE REGISTRY

Property values tagged with IC are from the ZIC/VINITI data file
provided by InfoChem.

STRUCTURE FILE UPDATES: 1 AUG 2005 HIGHEST RN 857935-17-2
DICTIONARY FILE UPDATES: 1 AUG 2005 HIGHEST RN 857935-17-2

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TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

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conducting SmartSELECT searches.

*
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

Structure search iteration limits have been increased. See HELP SLIMITS
for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
<http://www.cas.org/ONLINE/DBSS/registryss.html>

FILE HCAPLUS

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PASSWORD:

* * * * * RECONNECTED TO STN INTERNATIONAL * * * * * S

=> d his

(FILE 'HOME' ENTERED AT 09:23:47 ON 02 AUG 2005)

FILE 'REGISTRY' ENTERED AT 09:23:53 ON 02 AUG 2005

L1 26021 S EGEG/SQSP

FILE 'HCAPLUS' ENTERED AT 09:25:27 ON 02 AUG 2005

L2 4892 S L1

L3 643 S (FUSION OR CHIMER? OR CHIMAER?) (5A) PROTEIN? AND L2

L4 6 S L3 AND CAPTUR?

L5 0 S L3 AND POLYCATION?

L6 2 S L2 AND POLYCATION?

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L10 271887 S .{2-}(AG){0-8}EG{2-40}|| (AG){0-8}EG{2-40}..{2-}/SQSP

L11 271858 S SQL>=6 AND L10

FILE 'HCAPLUS' ENTERED AT 09:58:13 ON 02 AUG 2005

L12 32705 S L11

L13 10387 S L12 AND ?CATION?

FILE 'REGISTRY' ENTERED AT 10:01:10 ON 02 AUG 2005

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L16 26156 S L14 OR L15

FILE 'HCAPLUS' ENTERED AT 10:06:00 ON 02 AUG 2005

L17 4920 S L16

L18 2014 S L17 AND ?CATION?

L19 15 S L18 AND CAPTUR?

L20 25 S L18 AND SOLID(3A)SUPPORT?

L21 0 S L20 AND TAIL?

L22 44 S L18 AND TAIL?

L23 1 S L18 AND ?POLYMER?(3A)TAIL?

L24 3 S L18 AND TETHER?

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FILE 'REGISTRY' ENTERED AT 11:17:51 ON 02 AUG 2005

L30 1 S 775512-26-0

FILE 'HCAPLUS' ENTERED AT 11:25:29 ON 02 AUG 2005

FILE 'REGISTRY' ENTERED AT 11:27:21 ON 02 AUG 2005

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FILE 'HCAPLUS' ENTERED AT 11:46:33 ON 02 AUG 2005

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 L40 4 S L27 AND CATION(2A)BIND?
 L41 2 S L27 AND ?ANION?(2A)(BIND? OR BOUND?)
 L42 51 S L27 AND ?CATION?(2A)BIND?
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 L46 79 S L4 OR L6 OR L19 OR L24 OR L28 OR L29 OR L36-L45
 L47 13 S PY<2001 AND L46
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L48 TRA L47 1-13 RN : 4216 TERMS

FILE 'REGISTRY' ENTERED AT 12:11:25 ON 02 AUG 2005

L49 4216 SEA L48
 L50 58 S L49 AND L16

FILE 'HCAPLUS' ENTERED AT 12:13:54 ON 02 AUG 2005

L51 13 S L47 AND L50
 L52 846 S L17 AND (FUSION OR CHIMER? OR CHIMAER?)
 L53 302 S L52 AND BIND?
 L54 27 S L53 AND (IMMOBILIZ? OR IMMOBILIS?)
 L55 3 S L54 AND PY<2001
 SELECT RN L55 1-3

FILE 'REGISTRY' ENTERED AT 12:54:46 ON 02 AUG 2005

L56 69 S E1-E69
 L57 3 S L56 AND L16

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FILE 'HCAPLUS' ENTERED AT 12:56:27 ON 02 AUG 2005

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FILE COVERS 1907 - 2 Aug 2005 VOL 143 ISS 6
FILE LAST UPDATED: 1 Aug 2005 (20050801/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> s 157

L58 4 L57

=> s 157 and 155

4 L57

L59 3 L57 AND L55

=> d sqide 157 1-3

L57 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN

RN 283617-63-0 REGISTRY

CN Peptide (synthetic) fusion protein with green fluorescent protein (Aequorea victoria) fusion protein with peptide (synthetic linker) fusion protein with anti-(human chorionic gonadotropin α -subunit) immunoglobulin (Lama glama heavy chain V-D-J region) fusion protein with anti-(red reactive 6) immunoglobulin (Lama glama heavy chain V-D-J region) fusion protein with peptide (synthetic myc tag) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 44: PN: WO0040968 SEQID: 43 claimed protein

FS PROTEIN SEQUENCE

SQL 500

PATENT ANNOTATIONS (PNTE):

Sequence |Patent

Source |Reference

=====+=====

Not Given|WO2000040968

|claimed

|SEQID 43

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          =====
       101 FFKSAMPEGY VQERTIFFKD DGNYKTRAEV KFEGDTLVNR IELKGIDFKE
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       151 DGNILGHKLE YNYNSHNVYI MADKQKNGIK VNFKIRHNIE DGSVQLADHY
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       201 QQNTPIGDGP VLLPDNHLYS TQSALSKDPN EKRDHMLVLE FVTAAGITGG
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       251 SGGGGSSQVK LLESGGELVQ PGGSLKLSCA ASGLTFTNYS MGWFRPGPGV
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HITS AT: 1-500

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: BIOL (Biological study); PRP (Properties); USES
(Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L57 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN

RN 158935-45-6 REGISTRY

CN 5-13-Dynorphin B [5-methionine,6-alanine] (synthetic clone pLM138) fusion
protein with protein (synthetic 84-amino acid fragment) (9CI) (CA INDEX
NAME)

FS PROTEIN SEQUENCE

SQL 93

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HITS AT: 1-93

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L57 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2005 ACS on STN

RN 138361-59-8 REGISTRY

CN Laminin (human clone 129/123/7 A-subunit precursor protein moiety reduced)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN Laminin (human A-subunit precursor)

FS PROTEIN SEQUENCE

SQL 3075

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51 KLVEHVPGRP VRNPQCRICD GNSANPRERH PISHAIDGTN NWWQSPSIQN
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151 YYAVSDSECL SRYNITPRRG PPTYRADDEV ICTSYYSRLV PLEHGEIHTS
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651 KRQIDRDQLM TVLANVTHLL IRATYNSAKM ALYRLESVSL DIASSNAIDL
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751 CNVHGVCIAH AHNTTGVBCE QCLPGFYGEP SRGTPGDCQP CACPLTIASN
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851 CSGNVDPSEA GHCDSVTGEC LKCLGNTDGA HCERCADGFY GDAVTAKNCR
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901 ACECHVKGSH SAVCHLETGL CDCKPNVTGQ QCDQCLHGYY GLDSGHGCRP
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951 CNCSVAGSVS DGCTDEGQCH CVPGVAGKRC DRAHGFYAY QDGSCTPCDC
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1251 TSNFEPQVLI KGGRIRKQVI YMDAPAPENG VRQEQEVAMR ENFWKYFNSV
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1551 TDCVSCDDEC VGVLLNDLDE IGDAVLSLNL TGIIPVPYGI LSNLENTTKY
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1601 LQESLLKENM QKDLGKIKLE GVAEETDNLQ KKLTRMLAST QKVNATERI
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1651 FKESQDLAVA IERLQMSITE IMEKTTLNQT LDEDLLPNS TLQNMQNGT
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1701 SLLEIMQIRD FTQLHQATL ELKAAEDLLS QIQENYQKPL EELEVLKEAA
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1751 SHVLSKHNE LKAAEALVRE AEAKMQESNH LLLMVNANLR EFSDKKLHVQ
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1901 SAAYVHYNIQ SLIEESEELA RDAHRTVTET SLLSESLVSN GKAAVQRSSR
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1951 FLKEGNNLSR KLPGIALELS ELRNKTNRFQ ENAVEITRQT NESLLILRAI
=====
2001 PEGIRDKGAK TKELATSASQ SAVSTLRDVA GLSQELLNTS ASLSRVNTTL
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2051 RETHQLLQDS TMATLLAGRK VKDVEIQANL LFDRLKPLKM LEENLSRNLS
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2101 EIKLLISQAR KQAASIKVAV SADRDCIRAY QPQISSTNYN TLTLNVKTQE
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2151 PDNLLFYLGS STASDFLAVE MRRGRVAFW DLGSGSTRLE FPDFPIDDNR
=====
2201 WHSIHVARFG NIGSLSVKEM SSNQKSPTKT SKSPGTANVL DVNNSTLMFV
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2251 GGLGGQIKKS PAVKVTHFKG CLGEAFLNGK SIGLWNYIER EGKCRGCFGS
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2301 SQNEDPSFHF DSGSYSVVEK SLPATVTQII MLFNTFSPNG LLLYLGSYGT
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2351 KDFLSIELFR GRVKVMTDLG SGPITLLTDR RYNNGTWYKI AFQRNRKQGV
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2401 LAVIDAYNTS NKETKQGETP GASSDLNRLD KDPIYVGGLP RSRVVRRGVT
=====
2451 TKSFVGCIGN LEISRSTFDL LRNSYGVVRKG CLLEPIRSVS FLKGGYIELP
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2501 PKSLSPESEW LVTFATTNSS GIILAALGGD VEKRGDREEA HVPFFSVMLI
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2551 GGNIEVHVNP GDGTGLRKAL LHAPTGTCSG QAHSISLVR NRRITVQLD
=====
2601 ENNPVEMKLG TLVESRTINV SNLYVGGIPE GEGTSLTMR RSFHGCIKNL
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2651 IFNLELLDFN SAVGHEQVDL DTCWLSERP K LAPDAEDSKL LREPRAFPEQ
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2701 CVVDAALEYV PGAHQFGLTQ NSHFILPFNQ SAVRKKLSVE LSIRTFASSG
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2751 LIYYMAHQNQ ADYAVLQLHG GRLHFMFDLG KGRTKVSHPA LLSDGKWHTV
=====
2801 KTDYVKRKG F ITVDGRES PM VTVVGDG TML DVEGLFYLG LPSQYQARKI
=====
2851 GNITHSIPAC IGDVTVNSKQ LDKDSPVSAF TVNRCYAVAQ EGTYFDGSGY
=====
2901 AALVKEGYKV QSDVNITLEF RTSSQNGVLL GISTAKVDAI GLELVDGKVL
=====
2951 FHVNNAGARI TPAYEPKTAT VLCDGKWHTL QANKSKHRIT LIVDGNVAVG
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3001 ESPHTQSTSV DTNNPIYVGG YPAGVKQKCL RSQTSFRGCL RKLALIKSPQ
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3051 VQSFD FSRAF ELHGVFLHSC PGTES
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HITS AT: 1-3075

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPATFULL

DT.CA Caplus document type: Journal; Patent

RL.P Roles from patents: BIOL (Biological study); PROC (Process); PRP

(Properties); USES (Uses)
 RL.NP Roles from non-patents: PRP (Properties)
 2 REFERENCES IN FILE CA (1907 TO DATE)
 2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

=> d 150 sqide 1-58
 YOU HAVE REQUESTED DATA FROM FILE 'REGISTRY' - CONTINUE? (Y)/N:y

L50 ANSWER 1 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 482390-90-9 REGISTRY
 CN Green fluorescent protein [65-glycine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
 DT.CA Caplus document type: Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 2 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-46-3 REGISTRY
 CN Green fluorescent protein [65-glycine,68-leucine,72-alanine] (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
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HITS AT: 1-238
 MF Unspecified

CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 3 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-45-2 REGISTRY
CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,148-glycine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
=====

51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
=====

101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSGNV
=====

151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====

201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
=====

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 4 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-44-1 REGISTRY
CN Green fluorescent protein [65-glycine,72-alanine,203-tryptophan] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
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51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
=====

101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHN
=====

151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
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201 LSWQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
=====

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN,
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 5 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-43-0 REGISTRY
CN Green fluorescent protein [65-glycine,68-leucine,69-lysine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTCLKFICTT
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51 GKLPVPWPTL VTTFGYGLKC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
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101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
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151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====
201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 6 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-42-9 REGISTRY
CN yGreen fluorescent protein [65-leucine,65-glycine,72-alanine,203-tyrosine]
(Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTCLKFICTT
=====
51 GKLPVPWPTL VTTFGYGVQC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
=====
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
=====
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====
201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 7 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-41-8 REGISTRY
CN Green fluorescent protein [65-threonine,203-tyrosine] (Aequorea victoria)
(9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
=====
51 GKLPVPWPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
=====
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
=====
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====
201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 8 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-40-7 REGISTRY
CN Green fluorescent protein [65-threonine,203-histidine] (Aequorea victoria)
(9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
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51 GKLPVPWPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
=====
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
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151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
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201 LSHQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 9 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-39-4 REGISTRY
CN Green fluorescent protein [72-alanine,145-phenylalanine,203-leucine]
(Aequorea victoria) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Sapphire protein (Aequorea victoria mutant)
FS PROTEIN SEQUENCE
SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFYGVQC  FARYPDHMKR HOFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHNV
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSLQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 10 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-38-3 REGISTRY
CN Green fluorescent protein [65-glycine,72-alanine,79-arginine,203-tyrosine]
(Aequorea victoria) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Topaz protein (Aequorea victoria mutant)
FS PROTEIN SEQUENCE
SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFYGVQC  FARYPDHMRR HOFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
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       201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238
MF Unspecified

CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Cplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 11 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-37-2 REGISTRY
CN Green fluorescent protein [66-tryptophan] (Aequorea victoria) (9CI) (CA
INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
=====
51 GKLPVPWPTL VTTFSWGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
=====
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
=====
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====
201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDLYK
=====

HITS AT: 1-238
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Cplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 12 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-36-1 REGISTRY
CN Green fluorescent protein [66-phenylalanine] (Aequorea victoria) (9CI)
(CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

SEQ 1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
=====
51 GKLPVPWPTL VTTFSFGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
=====
101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
=====
151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
=====
201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDLYK
=====

HITS AT: 1-238
MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 13 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-35-0 REGISTRY
CN Green fluorescent protein [65-leucine] (Aequorea victoria) (9CI) (CA
INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
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          51 GKLPVPWPTL VTTFLYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
          151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 14 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-34-9 REGISTRY
CN Green fluorescent protein [65-cysteine] (Aequorea victoria) (9CI) (CA
INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
          51 GKLPVPWPTL VTTFCYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
          151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 15 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-33-8 REGISTRY
 CN Green fluorescent protein [54-alanine] (Aequorea victoria) (9CI) (CA
 INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLAVPWPTL VTTFYGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
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HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 16 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-32-7 REGISTRY
 CN Green fluorescent protein [64-leucine,65-threonine] (Aequorea victoria)
 (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTLTYGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNH
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)

. 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 17 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-31-6 REGISTRY
 CN Green fluorescent protein [65-threonine,72-alanine,149-lysine,153-threonine,167-threonine] (Aequorea victoria) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN Emerald protein (Aequorea victoria mutant)
 FS PROTEIN SEQUENCE
 SQL 238

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SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFTYGVQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHKV
          =====
       151 YITADKQKNG IKVNFKTRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
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HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
 DT.CA Caplus document type: Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 18 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-30-5 REGISTRY
 CN Green fluorescent protein [65-threonine,153-alanine,238-glutamic acid]
 (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
       151 YIAADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYE
          =====
```

HITS AT: 1-238

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
 DT.CA Caplus document type: Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 19 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-29-2 REGISTRY
CN Green fluorescent protein [64-leucine,65-threonine,66-tryptophan,146-isoleucine,153-threonine,163-alanine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
          51 GKLPVPWPTL VTTLTWGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYISHNV
          =====
          151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 20 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-28-1 REGISTRY
CN Green fluorescent protein [65-alanine,66-tryptophan,72-alanine,146-isoleucine,153-threonine,163-alanine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
          51 GKLPVPWPTL VTTFWGVQC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYISHNV
          =====
          151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 21 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-27-0 REGISTRY
CN Green fluorescent protein [66-tryptophan,123-valine,145-histidine,148-arginine,153-threonine,163-alanine,212-lysine] (Aequorea victoria) (9CI)
(CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFSWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRVELKGIDF KEDGNILGHK LEYNHNSRNV
          =====
       151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PKEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 22 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN 481774-26-9 REGISTRY
CN Green fluorescent protein [66-tryptophan,146-isoleucine,153-threonine,163-alanine,212-lysine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFSWGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRVELKGIDF KEDGNILGHK LEYNYISHNV
          =====
       151 YITADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PKEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 23.OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-25-8 REGISTRY
 CN Green fluorescent protein [66-histidine,145-phenylalanine,163-alanine]
 (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

```

SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHNV
          =====
       151 YIMADKQKNG IKANFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDLYK
          =====

```

HITS AT: 1-238
 MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
 DT.CA Caplus document type: Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 24 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-24-7 REGISTRY
 CN Green fluorescent protein [66-histidine,145-phenylalanine] (Aequorea
 victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

```

SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
        51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
       101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNFNSHNV
          =====
       151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
       201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDLYK
          =====

```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
 DT.CA Caplus document type: Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 25 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-23-6 REGISTRY

CN Green fluorescent protein [66-histidine] (Aequorea victoria) (9CI) (CA
INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
      51 GKLPVPWPTL VTTFSHGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
     101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
     151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
     201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 26 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN **481774-22-5** REGISTRY
CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,148-
glutamine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)
FS PROTEIN SEQUENCE
SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT
          =====
      51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDFFKSAMPE GYVQERTIFF
          =====
     101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSQNV
          =====
     151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
     201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL
DT.CA Caplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 27 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
RN **481774-21-4** REGISTRY

CN Green fluorescent protein [65-glycine,68-leucine,72-alanine,203-tyrosine]
(Aequorea victoria) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Yellow fluorescent protein (Aequorea victoria mutant)

FS PROTEIN SEQUENCE

SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTCLKFICTT
          =====
          51 GKLPVPWPTL VTTFGYGLQC FARYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
          151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSYQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 28 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 481774-20-3 REGISTRY

CN Green fluorescent protein [65-threonine] (Aequorea victoria) (9CI) (CA
INDEX NAME)

FS PROTEIN SEQUENCE

SQL 238

```
SEQ      1 MSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTCLKFICTT
          =====
          51 GKLPVPWPTL VTTFTYGVQC FSRYPDHMKR HDEFFKSAMPE GYVQERTIFF
          =====
          101 KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYNSHNV
          =====
          151 YIMADKQKNG IKVNFKIRHN IEDGSVQLAD HYQQNTPIGD GPVLLPDNHY
          =====
          201 LSTQSALSKD PNEKRDHMLV LEFVTAAGIT HGMDELYK
          =====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Caplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 29 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-19-0 REGISTRY
 CN Green fluorescent protein [endo-1a-valine,65-glycine,72-alanine,203-tyrosine] (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 239

```
SEQ      1 MVSKEELFT  GVPILVELD  GDVNGHKFSV  SGEGEDATY  GKLTCLKFICT
=====
      51 TGKLPVPWPT  LVTTFGYGVQ  CFARYPDHMK  RHDFFKSAMP  EGYVQERTIF
=====
     101 FKDDGNYKTR  AEVKFEGDTL  VNRIELKGID  FKEDGNILGH  KLEYNYNSHN
=====
     151 VYIMADKQKN  GIKVNFKIRH  NIEDGSVQLA  DHYQQNTPIG  DGPVLLPDNH
=====
     201 YLSYQSALS  DPNEKRDHNV  LLEFVTAAGI  THGMDELYK
=====
```

HITS AT: 1-239

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 PREP (Preparation); PRP (Properties); USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 30 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 481774-18-9 REGISTRY
 CN Green fluorescent protein (Aequorea victoria) (9CI) (CA INDEX NAME)
 FS PROTEIN SEQUENCE
 SQL 238

```
SEQ      1 MSKEELFTG  VVPILVELDG  DVNGHKFSVS  GEGEGDATYG  KLTCLKFICTT
=====
      51 GKLPVPWPTL  VTTFYGVQC  FSRYPDHMKR  HDFFKSAMPE  GYVQERTIFF
=====
     101 KDDGNYKTRA  EVKFEGDTLV  NRIELKGIDF  KEDGNILGHK  LEYNYNSHNV
=====
     151 YIMADKQKNG  IKVNFKIRHN  IEDGSVQLAD  HYQQNTPIGD  GPVLLPDNHY
=====
     201 LSTQSALSKD  PNEKRDHNV  LEFVTAAGIT  HGMDELYK
=====
```

HITS AT: 1-238

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER, USPAT2, USPATFULL

DT.CA Cplus document type: Patent

RLD.P Roles for non-specific derivatives from patents: ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PRP (Properties);
 USES (Uses)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 31 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 325868-75-5 REGISTRY
 CN Protein No55 (human DU145 cell cell nucleolus-associated gene No55) (9CI)
 (CA INDEX NAME)

OTHER NAMES:

CN GenBank CAC16786
 CN GenBank CAC16786 (Translated from: GenBank AJ250583)
 CN Nucleolar protein No55 (human DU145 cell gene No55)
 FS PROTEIN SEQUENCE
 SQL 437

```

SEQ      1 MARVAWGLLW LLLGSAGAQY EKYSFRGFPP EDLMPLAAAY GHALEQYEGE
          =====
      51 SWRESARYLE AALRLHRLLR DSEAFCHANC SGPAPAAKPD PDGGRADEWA
          =====
     101 CELRLFGRVL ERAACLRRCK RTLPAFQVPY PPRQLLRDFQ SRLPYQYLHY
          =====
     151 ALFKANRLEK AVAAAYTFLQ RNPKEHETAK YLNYYRGMLD VADESITDLE
          =====
     201 AQPYEAVFLR AVKLYNSGDF RSSTEDMERA LSEYLAVFAR CLAGCEGAHE
          =====
     251 QVDFKDFYPA IADLFAESLQ CKVDCEANLT PNVGGFYFVDK FVATMYHYLQ
          =====
     301 FAYYKLNDVR QAARSAASYM LFDPKDSVMQ QNLVYYRFHR ARWGLEEEEDF
          =====
     351 QPREEAMLYH NQTAELELL EFTHMYLQSD DEMELEETEP PLEPEDALSD
          =====
     401 AEFEGEGDYE EGMYADWWQE PDAKGDEAEA EPEPELA
          =====
  
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HITS AT: 1-437

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 32 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 296363-99-0 REGISTRY

CN G-protein coupled receptor VLGR1 (human precursor) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAD55586
 CN GenBank AAD55586 (Translated from: GenBank AF055084)
 CN Very large G-protein coupled receptor-1 (human precursor)
 FS PROTEIN SEQUENCE
 SQL 1967

```

SEQ      1 MQLCIFCCCC ILFYFDLYDF GRGYDFTIQE NGLQIDQPPE IGNISIVRII
          =====
      51 IMKNDNAEGI IEFDPKYTAF EVEEDVGLIM IPVVRHLGTY GYVTADFISQ
          =====
     101 SSSASPGGVD YILHGSTVTF QHGQNLSFIN ISIIDDNESE FEEPIEILLT
          =====
     151 GATGGAVLGR HLVSRIIIAK SDSPFGVIRF LNQSKISIAN PNSTMILSLV
          =====
     201 LERTGGLLGE IQVNWETVGP NSQEALLPQN RDIADPVSGL FYFGEGEGGV
          =====
     251 RTIILTIYPH EEIEVEETFI IKLHLVKGEA KLDSRAKDVT LTIQEFQDPN
          =====
  
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```

301 GVVQFAPETL SKKTYSEPLA LEGPLLITFF VRRVKGTFFE IMVYWELSSE
=====
351 FDITEDFLST SGFFTIADGE SEASFDVHLL PDEVPEIEED YVIQLVSVEG
=====
401 GAELDLEKSI TWFSVYANDD PHGVFALYSD RQSILIGQNL IRSIQINITR
=====
451 LAGTFGDVAV GLRISSDHKE QPIVTENAER QLVVKDGATY KVDVVPKKNQ
=====
501 VFSLSGSNFT LQLVTVMLVG GRFYGMPTIL QEAKSAVLPV SEKAANSQVG
=====
551 FESTAFLQMN ITAGTSHVMI SRRGTYGALS VAWTTGYAPG LEIPEFIVVG
=====
601 NMTPTLGSL SFSHGQRKGV FLWTFPSPGW PEAFLVHLHG VQSSAPGGAQ
=====
651 LRSGFIVAEI EPMGVFQFST SSRNIIVSED TQMIRLHVQR LFGFHSDLIK
=====
701 VSYQTTAGSA KPLEDFEPVQ NGELFFQKFQ TEVDFEITII NDQLSEIEEF
=====
751 FYINLTSVEI RGLQKFDVNW SPRLNLDFS AVITILDND LAGMDISFPE
=====
801 TTVAVAVDTT LIPVETESTT YLSTSKTTTI LQPTNVVAIV TEATGVSAIP
=====
851 EKLVTLHGTP AVSEKPDVAT VTANVSIHGT FSLGPSIVYI EEEMKNGTFN
=====
901 TAEVLIRRTG GFTGNVSITV KTFGERCAQM EPNALPFRGI YGISNLTWAV
=====
951 EEEDFEEQTL TLIFLDGERE RKVSVQILDD DEPEGQEFFY VFLTNPQGGG
=====
1001 QIVEGKDDTG FAAFAMVIIT GSDLHNGIIG FSEESQSGLE LREGAVMRRL
=====
1051 HLIVTRQPNR AFEDVKVFWR VTLNKTVVVL QKDGVNLMEE LQSVSGTTTC
=====
1101 TMGQTKCFIS IELKPEKVPQ VEVYFFVELY EATAGAAINN SARFAQIKIL
=====
1151 ESDSQSLVY FSVGSRLAVA HKKATLISLQ VARDSGTGLM MSVNFSTQEL
=====
1201 RSAETIGRTI ISPAISGKDF VITEGTLVFE PGQRSTVLDV ILTPETGSLN
=====
1251 SFPKRQIVL FDPKGGARID KVYGTANITL VSDADSQAIW GLADQLHQPV
=====
1301 NDDILNRVLH TISMKVATEN TDEQLSAMMH LIEKITTEGK IQAFSVASRT
=====
1351 LFYEILCSLI NPKRKDTRGF SHFAEVTENF AFSLLTNVTC GSPGEKSKTI
=====
1401 LDSCPYSIL ALHWYPQQIN GHKFEGKEGD YIRIPERLLD VQDAEIMAGK
=====
1451 STCKLVQFTE YSSQWFISG NNLPTLKNKV LSLSVKGQSS QLLTNDNEVL
=====
1501 YRIYAAEPRI IPQTSCLLW NQAAASWLSQ SQFCKVIEET ADYVECACSH
=====
1551 MSVYAVYART DNLSSYNEAF FTSGFICISG LCLAVLSHIF CARYSMFAAK
=====
1601 LLTHMMAASL GTQILFLASA YASPQLAEES CSAMAAVTHY LYLCQFSWML
=====
1651 IQSVNFWYVL VMNDEHTERR YLLFFLLSWG LPAFVVILLI VILKGIYHQS
=====
1701 MSQIYGLIHG DLCFIPNVYA ALFTAALVPL TCLVVVFVVF IHAYQVKPQW
=====
1751 KAYDDVFRGR TNAAEIPLIL YLFALISVTW LWGGLHMAYR HFWMLVLFVI
=====

```

```

1801 FNSLQGLYVF MUYFILHNQM CCPMKASYTV EMNGHPGPST AFFTPGSGMP
=====
1851 PAGGEISKST QNLIGAMEEV PPDWERASFQ QGSQASPDLK PSPQNGATFP
=====
1901 SSGGYQGSL IADEESQEFD DLIFALKTGA GLSVSDNESG QGSQEGGTLT
=====
1951 DSQIVELRRI PIADTHL
=====

```

HITS AT: 1-1967

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 33 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290872-78-5 REGISTRY

CN RTX toxin RtxA (Vibrio cholerae strain N16961 gene VC1451) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94608

CN GenBank AAF94608 (Translated from: GenBank AE004223)

FS PROTEIN SEQUENCE

SQL 4558

NTE

type	location	description
uncommon	Aaa-3773	-
uncommon	Aaa-3940	-
uncommon	Aaa-3948	-

```

SEQ      1 MVFYLIPIKRR VWLMGKPFWR SVEYFFTGNY SADDGNNNIV AIGFGGQIHA
=====
      51 YGGDDHVTVG SIGATVYTGS GNDTVVGGSA YLKVEDSTGH LIVKGAAGYA
=====
     101 DINKSGDGNV SFAGAAGGVS IDHLGNHGDV SYGGAAAYNG ITRKGLSGNV
=====
     151 TFAGAGGYNA LWHETNQGNL SFTGAGAGNK LDRTWSNRYQ GSHGDVTFDG
=====
     201 AGAANSISSR VETGNITFRG AGADNHLVRK GKVGDITLQG AGASNRIERT
=====
     251 HQAEDVYTQT RGNIRFEGVG GYNSLYSDVA HGDHIFSGGG AYNTIIRKGS
=====
     301 GNDFAKEGMT NAKADEIVLT KAVMSGSWG QDHHVTAVKS ASEPNTYLFA
=====
     351 FADSTYTKIN KVQLRNDPQT GELKYYSTAW YKEVNHLSNL ANQDISDNGG
=====
     401 FTAVNINGAY TLSDLKVEHQ QSVTVHAVEK SLTEYEWVTY ANGAVIDAKE
=====
     451 VSLSDAKMGG HAIYADGTKV DVKAVKSNRQ PNTYIYAKVL GPYTKIVVVE
=====
     501 LANDPETGAL KYQARSWYKE GDHTANIANQ DISSATGYNP MGKGGYSLSD
=====
     551 LHYSVNAVRS TSETVADIEE YTDQTLFKPA NDSGESSGDV RFNGAGGGNV
=====

```

601	IKSNVTRGNV	HFNGGGIANV	ILHSSQFGNT	EFNGGGAANV	IVKSGEEDL
651	TFRGAGLANV	LVHQSEQGKM	DVYAGGAVNV	LVRLGDGQYL	AHLLAYGNIS
701	VQKSGDSRV	VMLGGYNTHT	QIGSGNGLWL	AAGGFNVMTQ	VGKGDVA AVL
751	AGGANVLTKM	GEGELTSGML	GGANVITHIS	NDDQLSNTTA	VALGGANILT
801	KKKGKNTLAV	MGGGANVLTH	VGDGTTTGVM	VGGANILTKV	GNGDTTGILL
851	GVG NVLTHVG	DGQTLGVMGA	AGNIFTKVG D	GTSIAVMIGA	GNIFTHV GEG
901	NAWALMGGLG	NVFTKVGNGD	ALALMVAEAN	VFTHIGDGMS	VALMLAKGNV
951	ATKVGNGTTL	AAMVGNVNIF	THIGHGSTFA	AMIGQANIMT	KVGNDLTAAL
1001	MVGKANIMTH	VGDGTS LGLF	AGEVNVMTKV	GNGTTLAAMF	GKANIMTHVG
1051	DGLTGVLALG	EANIVTKLGD	DFMGVVA AAK	ANVVTHVGDA	TTAAVLAKGK
1101	NILTKVGE GT	TVGLLISDV G	NVMTHVGDGT	TIGIAKGKAN	LITKVG DGLG
1151	VNVTWGQANV	FTQVG DGD RY	NFAKGEANLI	TKVG D GQEV S	VVQGEANIIT
1201	HVGNGDDYTG	AWGKANVITK	VGHGQNVVLA	KGEANIVTQV	GDGDSFNALW
1251	SKGNI VTKVG	DGMQVTA A K G	QANITTTVGN	GLNVTAAYGD	ANINTKVG D G
1301	VSVNVAWGKY	NINTKVG DGL	NVAVMKGKAN	ANIHVG DGLN	INASYAQNNV
1351	AIKVGNGDFY	SLAVASSNTS	SNKLSALFDN	IKQTVLGVGG	SQAINYL VQG
1401	DEASSSGTHK	GRGAIATPEI	TKLDGFQMDA	IKEVSSDLGD	SLTGSVTKVD
1451	TPDLNKMQHA	LNVD DSSVQA	PNLIVNGDFE	LGEHGWQSTH	GVEASYAGSV
1501	YGVEGEHGHA	RVTELD TYTN	TSLYQDLANL	AQGEVIAVSF	DFAKRAGLSN
1551	NEGIEVLWNG	EVVFSSSGDE	SAWQQKNLKL	TAQAGSNRIE	FKGTGHNDGL
1601	GYILDNVVAT	SESSQQANAI	REHATQN PAA	QNALSDKERA	EADRQRLEQE
1651	KQKQLDAVAG	SQSQLEST DQ	QALENNGQAQ	RDAVKEESEA	VTAE LAKLAQ
1701	GLDVLDGQAT	HTGESGDQWR	NDFAGGLLDG	VQSQLDDAKQ	LANDKIAAAK
1751	QTLSDNNSKV	KESVAKSEAG	VAQGEQNRAG	VEQDIADAQA	DAEKRKADAL
1801	AKGKDAQQAE	SDAHHAVNNA	QSRGDRDVQL	AENKANQAQA	DAQGAKQNEG
1851	DRPDRQGVTG	SGLSGNAHSV	EGAGETDSHV	NTDSQTNADG	RFSEGLTEQE
1901	QEAL EGATNA	VNRLQINAGI	RAKNSVSSMT	SMFSETNSKS	IVVPTKVSPE
1951	PERQEVTRRD	VRISGVNLES	LSAVQGSQPT	GQLASKSVPG	FKSHFASTSI
2001	GIENELSGLV	VVLPKNSAQT	FGYVHDSQGN	PLFMLTKDMN	QGGYSNPVGI
2051	NDIQGVNNWQ	THTIELVTYP	SEISDTAAVE	SRKEAMLWLA	KEFTDHINQS

2101	NHQSLPHLVS	DDGRFTLVIS	NSKHLIAAGN	GTSIDAQGKT	IGMTPSGQQA
	=====	=====	=====	=====	=====
2151	TMAISAKEFG	TSSSPEVRLL	ESAPWYQAGL	RDEFLANAKN	TTLDDPATAQ
	=====	=====	=====	=====	=====
2201	NVYAYLTSVY	SKTADLAKEY	GIYINDWDPA	SEGFSPNAQG	LTDPKVKNAW
	=====	=====	=====	=====	=====
2251	SILPRTKPVR	MLELLSAEDS	RYVRQQIAEK	LKGTYESLSA	KNVFEYFQYG
	=====	=====	=====	=====	=====
2301	GEVAGHGINN	ATTGSVQQPE	PAILFEFRSV	PSALSDFVPK	TASTVKVDVK
	=====	=====	=====	=====	=====
2351	ALDHFDASASR	KAIITEVNAL	VSGSEDFDAW	YQEYRASKGQ	PPVKNPKSSA
	=====	=====	=====	=====	=====
2401	SANHKAEWLM	TQHAEQWAKI	TAPYTDNHET	LTSTKLASND	KEELHALGET
	=====	=====	=====	=====	=====
2451	SNLENNKQQE	NVASIINTML	NDMLPFYALR	TERNLLVQEG	DEGFEVRAWP
	=====	=====	=====	=====	=====
2501	GTEDKSKTII	LEDPEDAAQH	KAIERFILAN	FDNFEQMPDE	LFLVDNKVIS
	=====	=====	=====	=====	=====
2551	HHEGRTHVLA	QKVDGAWQYN	ATVELMSVTE	LLDAANVTGK	IRGESYQQVI
	=====	=====	=====	=====	=====
2601	DALTDYHASI	TEHADYEPES	VEKLLNLRKK	IEGYVLGHPD	SGRVEAMNSL
	=====	=====	=====	=====	=====
2651	LNQVNTRLDE	VSLLSVAEQT	IQAQNSFSRL	YDQLEAANLK	ESKHLYLDQN
	=====	=====	=====	=====	=====
2701	GDFVTKGKGN	LANIDLLGSR	EAVLEKVKLT	VSNEYGQTV	DTIFAGLSAK
	=====	=====	=====	=====	=====
2751	DLAKDGKGV	IAGLNKVHQA	IEQHLSPVSA	TLYIWKPSDH	SALGHAALQI
	=====	=====	=====	=====	=====
2801	GQGRTOLEGQ	AAADFNQQNY	VSWWPLGSKS	SNISNILNVA	TKDQPDCLKR
	=====	=====	=====	=====	=====
2851	WSDFSQPAHQ	NDTLEHDDAS	EENDGFGLHD	GDIKLRKFIE	KLNAAKGIDA
	=====	=====	=====	=====	=====
2901	SFKEASEGYA	SVLLGNPDML	ETTSIPAHVF	QPFVEQWNTD	SYDMMDVHR
	=====	=====	=====	=====	=====
2951	FAQELRLQAA	RSDDPELLEK	RIGNVIRQFA	ERALEEIEET	KASQADQGRV
	=====	=====	=====	=====	=====
3001	FRINLEGLDV	AAMQAEWHRL	SNDPDARYQL	LTKNCSSTVA	KVLKAGGADK
	=====	=====	=====	=====	=====
3051	LIGHTWLPKF	GVWTPTELFN	FGQALQEAQL	EIAAKKQSHQ	VTDVLDALSG
	=====	=====	=====	=====	=====
3101	NEKPKENVAI	ENDGTPPRDK	ESLSPLTRFL	NNELYGDKEA	RRKIGEITQT
	=====	=====	=====	=====	=====
3151	LLDHAWEKGE	SQKITLQGEA	GRLTGYHQQG	TAPSEGETSS	PSGKVVLFLH
	=====	=====	=====	=====	=====
3201	GSGSSAEQA	SAIRNHQKQ	GIDMLAVNLR	GYGESDGGPS	EKGLYQDART
	=====	=====	=====	=====	=====
3251	MFNYLVNDKG	IDPSNIIHGG	YSMGGPIAAD	LARYAAQNGQ	AVSGLLLDRP
	=====	=====	=====	=====	=====
3301	MPSMTKAITA	HEVANPAGIV	GAIAKAVNGQ	FSVEKNLEGL	PKETSILLLT
	=====	=====	=====	=====	=====
3351	DNEGLGNEGE	KLRTKLTAAG	YNVTGEQTFY	GHEASNRLMS	QYADQIVSGL
	=====	=====	=====	=====	=====
3401	SSSASVDEDL	DQQGLDTTST	KDQGISNKND	HLQVVDSEKA	LADGKILHNQ
	=====	=====	=====	=====	=====
3451	NVNSWGPITV	TPTTDGGETR	FDGQIIVQME	NDPVVAKAAA	NLAGKHAESS
	=====	=====	=====	=====	=====
3501	VVVQLDSDGN	YRVVYGDPK	LDGKLRWQLV	GHGRDHSETN	NTRLSGYSAD
	=====	=====	=====	=====	=====
3551	ELAVKLAKFQ	QSFNQAENIN	NKPDHISIVG	CSLVSDDKQK	GFGHQFINAM
	=====	=====	=====	=====	=====

```

3601 DANGLRVDVS VRSELAVDE AGRKHTKDAN GDWVQKAENN KVSLSWDAQG
=====
3651 EVVAKDERIR NGIAEGDIDL SRIGVNNVDE PARGAIGDNN DVFDAPEKRR
=====
3701 PETEVIANSS SSNQFSYSGN IQVNVGEGEF TAVNWGTSNV GIKVGTGGFK
=====
3751 SLAFGDNNVM VHIGDGESKH SVXIGGYQAL EGAQMFLGNR NVSFNFGHSN
=====
3801 DLILMDKSI PTPPLVNPFD GAARISGVLQ GIATSGEGED WLAAQEQQWT
=====
3851 LSGAKKFVKD MSGLDQSSSV DYTTLVELDS QNERDSRGLK HDAEATLNKQ
=====
3901 YNQWLSGNGN SGTSQLSRAD KLRQANEKLA FNFAVGGQGX DIQVTTGXWN
=====
3951 FMFGDNIQSI LDTNLGSLFG LMTQQFTATG QAKTTFTYTP QDLPRQLKNK
=====
4001 LLGQLAGVGA ETTLADIFGV DYTASGQIVS RNGQAVDGVA ILKEMLEVIG
=====
4051 EFSGDQLQAF VDPAKLLDSL KAGIDMGADG IKSFAETHGL KEKAPEEEKD
=====
4101 NSSSVVNGAN VNSAQGATVA DGNTETAETQ DRAFGFNSLN LPNLFATIFS
=====
4151 QDKQKEMKSL VENLKQNLTA DLLNMKEKTF DFLRNSGHLQ GDGDINISLG
=====
4201 NYNFWGGDG KDLGAYLGDN NNFWGGRGDD VFYATGKSNI FTGGEGNDMG
=====
4251 VLMGRENMMF GGDGNDTAVV AGRINHVFLG AGDDQS FVFG EGGEIDTGSG
=====
4301 RYVVTSGNF NRVDTGDDQD YSVTIGNNNQ VELGAGNDFA NIFGNYNRIN
=====
4351 AGAGNDVVKL MGYHAVLNGG DGDDHLIATA ISKFSQFNGG EGRDLMVLGG
=====
4401 YQNTFKGGTD VDSFVVSGDV IDNLVEDIRS EDNIVFNGID WQKLWFERSG
=====
4451 YDLKLSILRD PSNDSQSKF EHIGSVTFSD YFNGNRAQVV IGMSEKDLSG
=====
4501 EREYTMLSDS AIDALVQAMS GFEPQAGDNG FIDSLESKSQ AAISMAWSDV
=====
4551 VHKKGLMV
=====

```

HITS AT: 1-4558

****RELATED SEQUENCES AVAILABLE WITH SEQLINK****

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 34 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290417-48-0 REGISTRY

CN 5'-Nucleotidase (Vibrio cholerae strain N16961 gene VCA0545) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96447

CN GenBank AAF96447 (Translated from: GenBank AE004385)

FS PROTEIN SEQUENCE

SQL 580

```

SEQ      1 MPMRRKNQPA SITLAHINDT HSYFEPTSLQ LTLEHDADIL KPFVSAGGFA
          =====
          51 RIATRIAQLR DDAQRMQREF LFLHAGDCFQ GTLYFSLFKG KANADMLNAL
          =====
          101 KLDAMAIGNH ELDMGNYPPVA QFAQRIQFPL LAGNWDLSQE RDSKSLRLGS
          =====
          151 NPKVYSYDAL QGHARWIEKK AQGERIAIFG LSIDKMADIA NPDSPTPFVN
          =====
          201 AIETARKTIA AIHQHGINKI ILLSHLGYDG DIALAEQVSG ISLIVGGHSH
          =====
          251 VLQGDFSALG LGSQDEYGLK INHTYIVQAG FYALTGHGCH IDFAANGEVT
          =====
          301 RFEGRNELL L GRRMFVDASM SQEQISERYS QARDEVNDHP NVVVCKKDPV
          =====
          351 VQSLLOEKYI PQVRQLQQOI IAHADRTL RH LRIPDAEGGS EIAPLVAKAF
          =====
          401 VYALNKRGLD VQFAIHNAGG VRTSILPGSI SVADVAGKLL PFAVPIGVYQ
          =====
          451 VKGEVIARAL EGAINNALSN GVQGTGSGSY PYCHHLRYQY LADKPIGQRI
          =====
          501 TQLQIQLDGE WQAVDSEALY WGTSSAYTMK GKEGYDALLD MEGEGMVTQI
          =====
          551 SMADAFIELL SDCPSLLSFE AHDACECHHH
          =====

```

HITS AT: 1-580

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 35 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290417-17-3 REGISTRY

CN Protein (Vibrio cholerae strain N16961 gene VCA0510) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96413

CN GenBank AAF96413 (Translated from: GenBank AE004381)

FS PROTEIN SEQUENCE

SQL 968

```

SEQ      1 MTHYQTEIGK IMYSSHQCKR LSIMAILGCL PFSVNGAVES MPLMGGVYNS
          =====
          51 AHVFKHQITN SLSYSTRLTR DTALFTIAGL TLDSYILTL P LDVKTARVI
          =====
          101 KQISDPSYAI PLGYFLYQYY DRYTGMATED QFKNYLSTVY DEPALKGFEH
          =====
          151 SLFQLGKPVV TEQSQHSKDQ AHQEGIKVDS EFIATMTVLY DALVQIGEW R
          =====
          201 DLKQLPSQYQ YLSDTPADNA LVSKIQPLVV DILRQTANGM DEGEMKHALL
          =====
          251 SVLEDAKPEN ANKVNNKAQA ITVSLIDFVR LNVLKGYRQF LYQEERTARL
          =====
          301 KEWLNKTLDS DPEQLVTFLT SQQQRRAVQ VTV DGLQQGL IEGLVHPENP
          =====

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```

351 FIKQVYAEHQ QAEKNQHSTL MEPLHKKQV RFLSTLAEQN YQDPYYLPFF
=====
401 KQLYQHYRQT IVQVGISSTP TISVRNLPII KTGAKVSGLG GTGIPNFHFV
=====
451 DRQADRAYYF FGNDALQLDR LVNERGVKTM FDRLDYLKTL NCNAQYDWNA
=====
501 HTTYDGLVNL GAGEALRDFG EKRCRELNE RAEEERQLTA LRAKLIEQIT
=====
551 AYQNSSKWMV LTRATLKQRL EQQLAEYAER DIFGMPDYTL IYNPWPDHFA
=====
601 HFAGPFSDEV IMPTGELNRL DYWLRETEAA YKKAGIYERT LWGMAGDHGL
=====
651 APVYGTLNPE RKIFESLQKD LGIKIALEKI SSDEGEGPKL TNALNAPSYQ
=====
701 KIDVVVASTA GGNFMLDFFN SAAGWATQPI YQELTQWQPK ESDKPLDIVS
=====
751 ESLVRLGDSL DYLVVREKTC TVDDCAVRVI GMREGLRLDE IIRLVGNKRF
=====
801 YTSQQGQPQL LQLQQLNPYL PKPQANALEE FAQLVDKCLY RAEEANIATW
=====
851 CDEQEWRLT RFTPRPDSVN QLAALYEEDR AGTMNLFQPK GVGYNKVPK
=====
901 RHAGESYLEK DAFLGFWGKP IGPNAMALQS EQNGSLAPTL YEYLTGESIE
=====
951 AGHDGWGYPS LLNKLDIQ
=====

```

HITS AT: 1-968

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 36 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN **290415-80-4** REGISTRY

CN Threonyl-tRNA synthetase (Vibrio cholerae strain N16961 gene VCA0287)
(9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF96196

CN GenBank AAF96196 (Translated from: GenBank AE004368)

FS PROTEIN SEQUENCE

SQL 642

```

SEQ. 1 MPIITLPDGS QRHFDNPVST LEVAQSIGPG LAKATIAGRV NGARVDACDL
=====
51 IEHDASLEII TTKDEV DGLE IVRHSCAHL GHALKQLYPN AKMAIGPTID
=====
101 SGFYDIDLE QSLSQEDLEK IEARMVELAK TKYAVVKKKV SWQEARDTFE
=====
151 SRGESYKMEI LDENVARD DR PGLYHHEEYI DMCGRPHVPH MGFCQNFKLL
=====
201 NIAGAYWRGN SDNKMLQRIY GTAFHDKKAL QAHLTRLEEA AKRDHRKIGK
=====
251 QLDFHMQQE APGMVFWHHN GWSIFRDLEI FIRQKLNEYG YQEVKGPLMM
=====
301 DRVLWERSGH WDKYADAMFT TSSENREYAI KPMNCPGHIQ IFNQGLKSYR
=====

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```

351 DLPLRMAEFG SCHRNEPSGS LHGIMRVRGF TQDDAHIFCT EDQIQQEVTS
=====
401 CIKMVYDITYT TFGFQNIIVVK LSTRPEKRVG SDEIWDKSEQ ALIDSLKAMD
=====
451 IPFEIQEGEG AFYGPKEIEFT LYDCLDRAWQ CGTVQLDFNL PTRLGATYVG
=====
501 ESNERLIPVM IHRAILGSLE RFIGILIEEY AGFFPTWLAP EQAVVVNITD
=====
551 KQADYAHEVA QKLQKCGIRA KADLRNEKIG FKIREHTLKR VPYMLVCGDQ
=====
601 EMEAGEIAVR TRKGKDLGKF KLDDFIAHIQ AEIASRKLNL EE
=====
=====

```

HITS AT: 1-642

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CPlus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 37 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290410-83-2 REGISTRY

CN Dehydrogenase, 3-isopropylmalate (Vibrio cholerae strain N16961 gene VC2491) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 3-Isopropylmalate dehydrogenase (Vibrio cholerae strain N16961 gene VC2491)

CN GenBank AAF95633

CN GenBank AAF95633 (Translated from: GenBank AE004318)

FS PROTEIN SEQUENCE

SQL 363

```

SEQ      1 MTDRDYKIAV LPGDGIGPEV MAQAHKVLDA IEQKHGIRFS REEHDVGGIA
=====
      51 IDNHGCPLPE STLRACEEAD AVLFGSVGGP KWEHLPPNEQ PERGALLPLR
=====
     101 KHQQLFCNLR PAQIHQGLEA FSPLRADISA RGFDIVVRE LTGGIYFGQP
=====
     151 KGREGEGAHE KAFDTEVYHR FEIERIARIA FESARLRRKK VCSIDKANVL
=====
     201 QSSILWREVV SEIAKEYPDV SLSHMYIDNA TMQLIKDPAQ FVMLCSNIF
=====
     251 GDILSDECAM ITGSMGMLPS ASMNESKFGL YEPAGGSAPD IAGKNIANPV
=====
     301 AQILSAALML RYSLGEEAAA RDIENAVSQA LAAGELTADL AGSKPALSTS
=====
     351 AMGDKIASYI LNS
=====
=====

```

HITS AT: 1-363

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CPlus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 38 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290410-70-7 REGISTRY
 CN Protein (Vibrio cholerae strain N16961 gene VC2476) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAF95618
 CN GenBank AAF95618 (Translated from: GenBank AE004317)
 FS PROTEIN SEQUENCE
 SQL 157

```
SEQ      1  MLSSGGLSLND KSWQALVFDY TNDGMGWPIG ALASAEQILL AMSAQLVDTD
          =====
          51  FELSLLLPEG EGEEALFELA DAVAEWINHF ISGLGLSGAN LKHASVEAKE
          =====
          101  ALEDLEEMSK LGIDEEDDLA EQAELLEQVI EHIKACVLVL HAEFGVKPEQ
          =====
          151  DTKPTVH
          =====
```

HITS AT: 1-157

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 39 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290408-81-0 REGISTRY
 CN Elongation factor Ts (Vibrio cholerae strain N16961 gene VC2259) (9CI)
 (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF95403

CN GenBank AAF95403 (Translated from: GenBank AE004297)

FS PROTEIN SEQUENCE

SQL 280

```
SEQ      1  MAVTAALVKE LRERTGAGMM ECKKALVETN GDIELAIENM RKSGAAKAAK
          =====
          51  KAGNIAAEGT IMIKEGEGIA ALVEVNCQTD FVAKDSNFVA FANQVTDAAAL
          =====
          101  ASKASVEELQ AQFEEARVAL VAKIGENINI RRVQYVEGEA LATYRHGDRI
          =====
          151  GVVVAGSADV ETLKHAVMHV AASRPEFLTP DDVPAEVLVAK EREVQVGIAM
          =====
          201  NEGKSKEIAE KMVEGRMKKF TGEVSLTGQP FVMEPKKTVG EILAEGKATV
          =====
          251  SAFIRLEVGE GIEKQEGLSF AEEVALAQKG
          =====
```

HITS AT: 1-280

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 40 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290407-23-7 REGISTRY
 CN Peptidase, insulinase family (Vibrio cholerae strain N16961 gene VC2072)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAF95218
 CN GenBank AAF95218 (Translated from: GenBank AE004281)
 FS PROTEIN SEQUENCE
 SQL 939

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SEQ      1 MVFCDSSLTL PIRRNAVHIS PNDTHQYRYI TLSNGLRRTL IQSPDVQKCA
          =====
        51 AALAVNVGHF DDPIERQGLA HYLEHMLFLG TEKYPKVGDF QTFISQHGGG
          =====
       101 NNAWTGTEHT CFFFDVLPNA FAKALDRFSQ FFIAPLFNAE ALDKERQAVD
          =====
       151 SEYKLKIKDE SRRLYQVQKE TINPQHFPFSK FSVGNQHTLG DRENSSIRDE
          =====
       201 IIEFYQSHYS AKLMTLSLIG SQSFDELEAW AERYFAAIPN PQORDIKPLPP
          =====
       251 FVDREHTGIL IQIEPLKEIR KLILAFPMPs TESYYQKKPL SYFAHLIGYE
          =====
       301 GEGSLLEALK EKGWITTLA GGGVSGSNYR EFAVSCVLTQ EGLDHSVDEII
          =====
       351 QSLFQTLNLI ATQGLQAWRY QEKRAVLESA FRFQETQRPL DMVSHLVVNM
          =====
       401 QHYAPEDTAY GDYMMSGYDE ALLLHILSYL TPENLRATLI AKGGEYDKKA
          =====
       451 QWYFTPYSVR PFTTEQLHRF RQPLDLPISL PEPNPFICYD LDPSEVKESH
          =====
       501 TLPQVLQDLP GFKLWHQQDT EFRVPKGVII VAIDSPHAVA NCRNIVMTRL
          =====
       551 CVEMFLDALA KETYQAEIAG MGYNLIAHQG GVTLTLSGFS QKLPLQMEVI
          =====
       601 LRKFAQRDFQ PKRFATIKQQ MTRNWRNAAH DKPISQLFNA MTGLLQPNNP
          =====
       651 PYAELLAAID DVQVEELAHF VDTILSQLHV EMFVYGDWPA AEAHKMAEVL
          =====
       701 KDALRVQGQT YEESLRPLVM LGKSGTFQRE VQCQQDDSAI VVYYQSHEVS
          =====
       751 PRSIALYSLA NHLMSATFFH EIRTKQQLGY MVGTGNMPLN RHPGLILYVQ
          =====
       801 SPSAPPSELI RSIDEFLNAL YMVLELNEY QWHSSKRGLW NQISAPDPTL
          =====
       851 RIRAQRLWVA IGKNDLSFDQ REKVLEELKN LSRADMIRFV VNELKPRTAH
          =====
       901 RLIMHTQGRA HHEAPALQLG QEIGSVEEFQ LRPKAYDVG
          =====
  
```

HITS AT: 1-939

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 41 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290404-95-4 REGISTRY
 CN Sigma-54 dependent transcriptional regulator (Vibrio cholerae strain N16961 gene VC1817) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94965
 CN GenBank AAF94965 (Translated from: GenBank AE004257)
 FS PROTEIN SEQUENCE
 SQL 587

```

SEQ      1 MMQLQQLSHV NWLVNSWQRS EQAGLTQQSR AQDIRLSDNK LKERRQELAG
          =====
      51 LIDTVSRFAL PLFYQLFAHS DSRLILTDQH GVIIGSWGQA RFREKLSQIA
          =====
     101 LSSGACWQEP IKGTNAIGTA LIEQKPISVI GEQHFIQHHH FISCASAPIF
          =====
     151 DYTGQLIGVL DITSEQQKHT LSTQVVVQNM VQLVENQLLN QIPHGHVRID
          =====
     201 LACEPSLLSS GWQGVIIADE SGQILAHNQV AGQLLAQGRV IGQSVEQVLP
          =====
     251 RPQTHASFIY TTTPLHSKQH RTRALTPASD LHFGDAEVER CWQQANRVID
          =====
     301 KDIRLLILGQ TGVGKNEFVK ALHKNSQRKN GPLVAVNCGA LAKELVEAEL
          =====
     351 FGYVAGAFTG ASHKG YQGVK RLADKGILFL DEIADLPLDA QSRLHLVLQD
          =====
     401 KTVLPVGSNH ATKVDIQIIA ATHKNLEQLV TQGLFRQDLY YRLSDLVVEL
          =====
     451 PSFQQRQDRQ ALIHIIHRRY SDAGQQICGD LMQRLLAYHW PGNLRELDL
          =====
     501 IKVASLMAEG EGVLTFTNHL THLAQKLSHA APTATEDDQQ KDIKSTVEAS
          =====
     551 LLKTYQATQG NISQTSRLLG LSRNTIYRKL KALGILK
          =====

```

HITS AT: 1-587

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CPlus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 42 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290402-60-7 REGISTRY
 CN Protein (Vibrio cholerae strain N16961 gene VC1555) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94709
 CN GenBank AAF94709 (Translated from: GenBank AE004233)
 FS PROTEIN SEQUENCE
 SQL 170

```

SEQ      1 MWRLRASSIN KETPMFIGHI TQRQFCAALS PQLQRLINEV LQRVAAPLPT
          =====
      51 GKHELQGDSA FFLVMEDHTQ PLALRRSECH ARYLDVQILL QGRERFGYSL
          =====
     101 APFSGLEDL LATRDVAFSA QLVEERFVDL AAGDFIVFYP GQPHRPLIAV
          =====

```

151 EGEGERPVRKV VIKVDKAFKE

=====

HITS AT: 1-170

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 43 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290401-24-0 REGISTRY

CN Protein (Vibrio cholerae strain N16961 gene VC1380) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94538

CN GenBank AAF94538 (Translated from: GenBank AE004217)

FS PROTEIN SEQUENCE

SQL 116

SEQ 1 MKASELKIL NQLPDDLDPD VVMGEVWLPE RLIEAQLDDD MLFLTFDNAP

=====

51 EEEGEEEEGR GFVEHEMELI RSQMTILAE DSGPKTKAEA LLALITLAHE

=====

101 RTSSEFIEIL GTMLEE

=====

HITS AT: 1-116

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 44 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 290398-85-5 REGISTRY

CN Heat shock protein HtpX (Vibrio cholerae strain N16961 gene VC1117) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN GenBank AAF94276

CN GenBank AAF94276 (Translated from: GenBank AE004192)

FS PROTEIN SEQUENCE

SQL 287

SEQ 1 MKRILLFLAT NLAVVLVLSV VLNIVYAVTG MQPGSLSGLL VMAAVFGFGG

=====

51 AFISLLMSKS MALRSVGGVV IDTPRNEMEH WLLETVRRQA NQAGIGMPTV

=====

101 AIYDAPDMNA FATGAKRDDS LVAVSTGLLH NMTRDEAEAV LAHEVSHIAN

=====

151 GDMVTMTLMQ GVVNTFVIFL SRFIANIVAS RDSEEGEGSN MMVYFGVSMV

=====

201 LELVFGFLAS FITMWYSRHR EFHADAGAAQ LVGKHKMIAA LERLKMGOES

=====

251 HLEGSMMAFG ITGKRSLSEL MMTHPPLEKR IAALRNM

=====

HITS AT: 1-287

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER
 DT.CA CAplus document type: Journal
 RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 45 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290395-16-3 REGISTRY
 CN Isoleucyl-tRNA synthetase (Vibrio cholerae strain N16961 gene VC0682)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAF93847
 CN GenBank AAF93847 (Translated from: GenBank AE004154)
 FS PROTEIN SEQUENCE
 SQL 949

```

SEQ      1 MSEYKDTLNL PETGFPMRGD LAKREPEMLQ RWYQEDLYGA IRQAKKGKKS
          =====
        51 FVLHDGPPYA NGDIHIGHAL NKILKDVIK SKTSLSGFDAP YIPGWDCHGL
          =====
       101 PIELMVEKKV GKPGQKVTA EFREKCREYA AGQVEGQKES FKRLGILGEW
          =====
       151 DKPYRTMDFV TEANIIRALG KIADNGHLLK GFKPVHWCTD CGSALAEAEV
          =====
       201 EYKNKVS PSI DVRFKADEA AVLAKFGLAA GHEGKGDVSI VIWTTTPWTL
          =====
       251 PANRAVCLRA DLEYVLIQVE GEQPERIIVA SELAKSVMDR AGIEHFHNLG
          =====
       301 FATGADLELV QFQHPFYSFT VPAILGDHVT TDSGTGVVHT APGHGQEDFA
          =====
       351 VGQQYGLEVA NPVGSNGVYL PDTELFAGQH VFKANDSVLE VLKEKGALLH
          =====
       401 HHAYEHSYPH CWRHKTPPIF RATPQWFVSM EQAGLREQAL TAIKGVHWMP
          =====
       451 DWGQSRIEGM VAGRPEWCIS RQRTWGVPIA LFBVKETAEL HPNSADLIEK
          =====
       501 VAQLVEQKGI QAWWDLDTAE LLGAEDAANY EKVLDTLDVW FDSGVTHSAV
          =====
       551 VDAQREFNGA EADMYLEGSD QHRGWFFQSSL ISSVAMKGKA PYKEVLTHGF
          =====
       601 VVDGQGRKMS KSIGNVVAPQ DVTNKLADI LRLWVASTDY TGEVAVSDEI
          =====
       651 LKRSADAYRR IRNTARFFLA NLNGFNPTTD IIPVEDMVAL DRWAVGRALA
          =====
       701 AQQEIIQAYQ DYNLHAVVQR LMNFCSIEMG SFYLDVIKDR QYTAKRGGHA
          =====
       751 QRSCQTALFF IVEALVRWMA PIMSFTADEI WNAMPAQQAD GSARDKFVFT
          =====
       801 TEWFDGLFGL AEGEELNNAF WNDIQKVRGS VNKLLNARN EKLIGGSLQA
          =====
       851 ELVLFADDSL ASKLAKLGDE LRFVLLT SKA VVKPLAEKSE AAQATDIDGL
          =====
       901 FVQVNKTEAE KCDRCWHHTP DVGTIAGHTT ICGRCVSNE GEGERVKFA
          =====

```

HITS AT: 1-949

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER
 DT.CA Caplus document type: Journal
 RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 46 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 290392-99-3 REGISTRY
 CN Dehydrogenase, malate (Vibrio cholerae strain N16961 gene VC0432) (9CI)
 (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAF93605
 CN GenBank AAF93605 (Translated from: GenBank AE004130)
 CN Malate dehydrogenase (Vibrio cholerae strain N16961 gene VC0432)
 FS PROTEIN SEQUENCE
 SQL 353

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SEQ      1 MRKVAKLTLI DCNQIVITIA FDGRIHLITL QTYKRLLSRR FTMKVAVIGA
          =====
        51 AGGIGQALAL LLKNRLPAGS DLALYDIAPV TPGVAADLSH IPTPVTIKGY
          =====
       101 AGEDPTPALE GADVVLVSAG VARKPGMDRA DLFNVNAGIV KALAEEKIAVV
          =====
       151 CPKACVGIIT NPVNTTVPIA AEVLKKAGVY DKRKLFGVTT LDVIRSETFV
          =====
       201 AALKDKDPGQ VRVPVIGGHS GVTILPLLSQ VEGVSFTDEE VAALTKRIQN
          =====
       251 AGTEVVEAKA GGGSATLSMG QAACRFGAL VKALQGESDV VEYAYVEGEG
          =====
       301 EYAPFFAQPI KLGKNGVEAL LDIGKLSAYE QAALDGMLDT LKGDIQIGVE
          =====
       351 FVK
          ===

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HITS AT: 1-353

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER
 DT.CA Caplus document type: Journal
 RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
 1 REFERENCES IN FILE CA (1907 TO DATE)
 1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 47 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 272763-00-5 REGISTRY
 CN Protein JSAP1d (JNK/SAPK-associated protein-1d) (mouse) (9CI) (CA INDEX
 NAME)
 OTHER NAMES:
 CN 13: PN: W00031132 SEQID: 12 claimed protein
 CN JNK/SAPK-associated protein 1d (mouse gene jsap1)
 CN JSAP1d protein (mouse)
 CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1)
 (mouse gene jsap1 isoform JSAP1d)
 FS PROTEIN SEQUENCE
 SQL 1336

PATENT ANNOTATIONS (PNTE):

Sequence | Patent
Source | Reference
=====+=====

Not Given | WO2000031132
| claimed
| SEQID 12

```

SEQ      1 MMEIQMDEGG GVVVYQDDYC SGSVMSERVS GLAGSIYREF ERLIHCYDEE
=====
    51 VVKELMPLVV NVLENLDSVL SENQEHEVEL ELLREDNEQL LTQYEREKAL
=====
   101 RKQAEKFIE FEDALEQEK ELQIQVEHYE FQTRQLELKA KNYADQISRL
=====
   151 EERESEMKKE YNALHQRHTE MIQTYVEHIE RSKMQQVGGS GQTESSLPGR
=====
   201 RKERPTSLNV FPLADGMVRA QMGGKLVPAQ DHWHLSDLGQ LQSSSSYQCP
=====
   251 NDEMSESGQS SAAATPSTTG TKSNTPTSSV PSAAVTPLNE SLQPLGDYVS
=====
   301 VTKNNKQARE KRNSRNMEVQ VTQEMRNVSI GMGSSDEWSD VQDIIDSTPE
=====
   351 LDVCPETRL E RTGSSPTQGI VNKAFGINTD SLYHELSTAG SEVIGDVDEG
=====
   401 ADLLGEFSVR DDFFGMGKEV GNLLLENSQL LETKNALNVV KNDLIAKVDQ
=====
   451 LSGEQEVLKG ELEAAKQAKV KLENRIKELE EELKRVKSEA VTARREPREE
=====
   501 VEDVSSYLCT ELDKIPMAQR RRFTRVEMAR VLMERNQYKE RLMELQEAVR
=====
   551 WTEMIRASRE HPSVQEKKKS TIWQFFSRLF SSSSSPPPAK RSYPSVNIHY
=====
   601 KSPTAAGFSQ RRSALCQIS AGSRPLEFFP DDDCTSSARR EQKREQYRQV
=====
   651 REHVRNDDGR LQACGWSLPA KYKQLSPNGG QEDTRMKNVP VPVYCRPLVE
=====
   701 KDPSTKLWCA AGVNLSGWKP HEEDSSNGPK PVPGRDPLTC DREGEGEPKS
=====
   751 THPSPEKKKA KETPEADATS SRVWILTSTL TTSKVVIIDA NQPGTIVDQF
=====
   801 TVCNAHVLCI SSIPAASDSD YPPGEMFLDS DVNPEDSGAD GVLGITLVG
=====
   851 CATRCNVPRS NCSSRGDTPV LDKGQGDVAT TANGKVNPSQ STEEATEATE
=====
   901 VPDGPSESE ATTVRPGPLT EHVFTDPAPT PSSSTQPASE NGSESNGTIV
=====
   951 QPQVEPSGEL STTTSSAAPT MWLGAQNGWL YVHSAVANWK KCLHSIKLKD
=====
  1001 SVLSLVHVKG RVLVALADGT LAIFHRGEDG QWDLSNYHLM DLGHPHHSIR
=====
  1051 CMAVVNDRVW CGYKNKVHVI QPKTMQIEKS FDAHPRRESQ VRQLAWIGDG
=====
  1101 VWVSIRLDST LRLYHAHTHQ HLQDV DIEPY VSKMLGTGKL GFSFVRITAL
=====
  1151 LIAGNRLWVG TGNGVVISIP LTETVVLHRG QLLGLRANKT SPTS GEGTRP
=====
  1201 GGIIHVGDD SSDKAASSFI PYCSMAQAQL CFHGHRDAVK FFVSVPGNVL
=====
  1251 ATLNGSVLDS PSEGPGPAAP AADAEGQKLG NALVLSGGEG YIDFRIGDGE
=====

```

1301 DDETEECAGD VNQTKPSLSK AERSHIIWQ VSYTPE

=====

HITS AT: 1-1336

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
OCCU (Occurrence); PRP (Properties); USES (Uses)RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP
(Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 48 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 272762-99-9 REGISTRY

CN Protein JSAP1c (JNK/SAPK-associated protein-1c) (mouse) (9CI) (CA INDEX
NAME)

OTHER NAMES:

CN 12: PN: WO0031132 SEQID: 11 claimed protein

CN JNK/SAPK-associated protein 1c (mouse gene jsap1)

CN JSAP1c protein (mouse)

CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1)
(mouse gene jsap1 isoform JSAP1c)

FS PROTEIN SEQUENCE

SQL 1337

PATENT ANNOTATIONS (PNTE):

Sequence |Patent

Source |Reference

=====+

Not Given|WO2000031132

|claimed

|SEQID 11

```

SEQ      1 MMEIQMDEGG GVVVYQDDYC SGSVMSERVS GLAGSIYREF ERLIHCYDEE
          =====
        51 VVKELMPLVV NVLENLDSVL SENQEHEVEL ELLREDNEQL LTQYEREKAL
          =====
       101 RKQAEKFFIE FEDALEQEKK ELQIQVEHYE FQTRQLELKA KNYADQISRL
          =====
       151 EERESEMCKE YNALHQRHTE MIQTYVEHIE RSKMQQVGGS GQTESSLPGR
          =====
       201 SRKERPTSLN VFPLADGMVR AQMGGKLVPA GDHWHLSDLG QLQSSSSYQC
          =====
       251 PNDEMSESGQ SSAAATPSTT GTKSNTPTSS VPSAAVTPLN ESLQPLGDYV
          =====
       301 SVTKNNKQAR EKRNSRNMEV QVTQEMRNVS IGMGSSDEWS DVQDIIDSTP
          =====
       351 ELDVCPETRL ERTGSSPTQG IVNKAFGINT DSLYHELSTA GSEVIGDVDE
          =====
       401 GADLLGEFSV RDDFFGMGKE VGNLLLENSQ LLETKNALNV VKNDLIAKVD
          =====
       451 QLSGEQEVLK GELEAAKQAK VKLENRIKEL EEELKRVKSE AVTARREPRE
          =====
       501 EVEDVSSYLC TELDKIPMAQ RRRFTRVEMA RVLMEQNQYK ERLMELQEAV

```

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=====
551 RWTEMIRASR EHPSVQEKKK STIWQFFSRL FSSSSSPPPA KRSYPSVNIH
=====
601 YKSPTAAGFS QRRSHALCQI SAGSRPLEFF PDDICTSSAR REQKREQYRQ
=====
651 VREHVRNDDG RLQACGWSLP AKYKQLSPNG GQEDTRMKNV PVPVYCRPLV
=====
701 EKDPSTKLWC AAGVNLSGWK PHEEDSSNGP KVPVGRDPLT CDREGEGERPK
=====
751 STHPSPEKKK AKETPEADAT SSRVWILTST LTTSKVVIID ANQPGTIVDQ
=====
801 FTVCNHVLVC ISSIPAASDS DYPPGEMFLD SDVNPEDSGA DGVLAGITLV
=====
851 GCATRCNVPR SNCSSRGDTP VLDKGQGDVA TTANGKVNPS QSTEEATEAT
=====
901 EVDPDGPSES EATTVRPGPL TEHVFTDPAP TPSSSTQPAS ENGSESNGTI
=====
951 VQPQVEPSGE LSTTTSSAAP TMWLGAQNGW LYVHSAVANW KKCLHSIKLK
=====
1001 DSVLSLVHVK GRVLVALADG TLAI FHRGED GQWDL SNYHL MDLGHPHHSI
=====
1051 RCMVVNDRV WCGYKNKVHV IQPKTMQIEK SFDHPRRES QVRQLAWIGD
=====
1101 GVWVSIRLDS TLRLYHAHTH QHLQDV DIEP YVSKMLGTGK LGFSFVRITA
=====
1151 LLIAGNRLWV GTGNGVVISI PLTETVVLHR GQLLGLRANK TSPTS GEGTR
=====
1201 PGGIIHVGVD DSSDKAASSF IPYCSMAQAQ LCFHGHRDAV KFFVSVPGNV
=====
1251 LATLNGSVLD SPSEGP GPAA PAADAEGQKL KNALVLSGGE GYIDFRIGDG
=====
1301 EDDETEECAG DVNQTKPSLS KAERSHIIWV QVSYTPE
=====

```

HITS AT: 1-1337

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PRP (Properties); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 49 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 272762-98-8 REGISTRY

CN Protein JSAP1b (JNK/SAPK-associated protein-1b) (mouse) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 11: PN: WO0031132 SEQID: 10 claimed protein

CN JNK/SAPK-associated protein 1b (mouse gene jsap1)

CN JSAP1b protein (mouse)

CN Protein JSAP1 (JNK/stress-activated protein kinase-associated protein 1) (mouse gene jsap1 isoform JSAP1b)

FS PROTEIN SEQUENCE

SQL 1314

PATENT ANNOTATIONS (PNTE):

Sequence	Patent
Source	Reference
Not Given	WO2000031132
	claimed
	SEQID 10

SEQ	1	MMEIQMDEGG	GVVVYQDDYC	SGSVMSESVS	GLAGSIYREF	ERLIHCYDEE
		=====	=====	=====	=====	=====
51	VVKELMPLVV	NVLENLDSVL	SENQEHEVEL	ELLREDNEQL	LTQYEREKAL	
		=====	=====	=====	=====	
101	RKQAEKFKIE	FEDALEQEKK	ELQIQVEHYE	FQTRQLELKA	KNYADQISRL	
		=====	=====	=====	=====	
151	EERESEMKKE	YNALHQRHTE	MIQTYVEHIE	RSKMQQVGGS	GQTESSLPGR	
		=====	=====	=====	=====	
201	SPRQSWRKSR	KERPTSLNVF	PLADGMCPND	EMSESGQSSA	AATPSTTGTK	
		=====	=====	=====	=====	
251	SNTPTSSVPS	AAVTPLNESL	QPLGDYVSVT	KNNKQAREKR	NSRNMEVQVT	
		=====	=====	=====	=====	
301	QEMRNVSIGM	GSSDEWSDVQ	DIIDSTPELD	VCPETRLERT	GSSPTQGIVN	
		=====	=====	=====	=====	
351	KAFGINTDSL	YHELSTAGSE	VIGDVDEGAD	LLGEFSVRDD	FFGMGKEVGN	
		=====	=====	=====	=====	
401	LLLENSQLLE	TKNALNVVKN	DLIAKVDQLS	GEQEVKLGEL	EAAKQAKVKL	
		=====	=====	=====	=====	
451	ENRIKELEEE	LKRVKSEAVT	ARREPREEVE	DVSSYLCTEL	DKIPMAQRRR	
		=====	=====	=====	=====	
501	FTRVEMARVL	MERNQYKERL	MELQEAVRWT	EMIRASREHP	SVQEKKKSTI	
		=====	=====	=====	=====	
551	WQFFSRLFSS	SSSPPPAKRS	YPSVNIHYKS	PTAAGFSQRR	SHALCQISAG	
		=====	=====	=====	=====	
601	SRPLEFFPDD	DCTSSARREQ	KREQYRQVRE	HVRNDDGRLQ	ACGWSLPAKY	
		=====	=====	=====	=====	
651	KQLSPNGGQE	DTRMKNPVPV	VYCRPLVEKD	PSTKLWCAAG	VNLSGWKPHE	
		=====	=====	=====	=====	
701	EDSSNGPKPV	PGRDPLTCDR	EGEGEPKSTH	PSPEKKKAKE	TPEADATSSR	
		=====	=====	=====	=====	
751	VWILTSTLTT	SKVVIIDANQ	PGTIVDQFTV	CNAHVLCISS	IPAASDSDYP	
		=====	=====	=====	=====	
801	PGEMFLDSDV	NPEDSGADGV	LAGITLVGCA	TRCNVPRSNC	SSRGDTPVLD	
		=====	=====	=====	=====	
851	KGQGDVATTA	NGKVNPSQST	EEATEATEVP	DPGPSESEAT	TVRPGPLTEH	
		=====	=====	=====	=====	
901	VFTDPAPTPS	SSTQPASENG	SESNGTIVQP	QVEPSGELST	TTSSAAPTMTW	
		=====	=====	=====	=====	
951	LGAQNGWLYV	HSAVANWKKC	LHSIKLKDSV	LSLVHVKGRV	LVALADGTLA	
		=====	=====	=====	=====	
1001	IFHRGEDGQW	DLSNYHLM DL	GHPHHSIRCM	AVVNDRVWCG	YKNKVHVIQP	
		=====	=====	=====	=====	
1051	KTMQIEKSF	AHPRRESQVR	QLAWIGDGVW	VSIRLDSTLR	LYHAHATHQHL	
		=====	=====	=====	=====	
1101	QDVDIEPYVS	KMLGTGKLGF	SFVRITALLI	AGNRLWVG TG	NGVVISIPLT	
		=====	=====	=====	=====	
1151	ETVVLHRGQL	LGLRANKTSP	TSGEGTRPGG	IIHVGDDSS	DKAASSFIPY	
		=====	=====	=====	=====	
1201	CSMAQAQLCF	HGHRDAVKFF	VSVPGNVLAT	LNGSVLDSPS	EGPGPAAPAA	
		=====	=====	=====	=====	

1251 DAEGQKLKNA LVLSGGEGYI DFRIGDGEDD ETEECAGDVN QTKPSLSKAE
 =====
 1301 RSHIIVWQVS YYPE
 =====

HITS AT: 1-1314

****RELATED SEQUENCES AVAILABLE WITH SEQLINK****

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS
 DT.CA Caplus document type: Journal; Patent
 RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 OCCU (Occurrence); PRP (Properties); USES (Uses)
 RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP
 (Properties)
 2 REFERENCES IN FILE CA (1907 TO DATE)
 2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 50 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN **258492-41-0** REGISTRY
 CN Enzyme (simian immunodeficiency virus strain SIVcpz gene pol precursor)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank AAF18575
 CN GenBank AAF18575 (Translated from: GenBank AF115393)
 CN Pol polyprotein (simian immunodeficiency virus strain SIVcpz gene pol)
 FS PROTEIN SEQUENCE
 SQL 1013
 NTE

type	location	description
uncommon	Aaa-471	-
uncommon	Aaa-489	-
uncommon	Aaa-575	-

```

SEQ      1 FFRERLVSVE RGIKETRELP AGQEGTHSSA PRELWVSGSN RKETGGGEGE
          =====
        51 GKGTPVSSVN LPQITLWQRP LLGVKIEGQL IEALLDTGAD DTVIDNVQLT
          =====
       101 GKWRPKMIGG IGGFIKVKQY DNIAIEIEGR KTTGTVLVGP TPVNIIGRNI
          =====
       151 LTQIGCTLNF PISPIETVPV KLKPGMDGPR VKQWPLTAEK IKALTEICQE
          =====
       201 MEKEGKISRI GPENPYNTPI FAIKKKDSTK WRKLVDREL NKRTQDFWEV
          =====
       251 QLGIPHPAGL KKKKSVTVLD VGDAYFSCPL DENFRKYTAF TIPSVNNETP
          =====
       301 GIRYQYNVLP QGWKGSPAIF QSSMIKILTP FRQHPDLII YQYMDDLIVG
          =====
       351 SDLELREHRE KVELLRQHLL TWGFTTPDKK HQKEPPFLWM GYELHPDKWT
          =====
       401 VQPIQLPQKE TWTVNDIQKL VGKLNWASQI YPGIKVKQLC KLIKGTKALT
          =====
       451 DIVTMTQAE MELEENREIL XDPVHGVYYD PEKELIAEQ KQNSQWQTYQ
          =====
       501 IFQEQHKNLK TGKYARQRSA HTNDIRQLAE VVQKIATESI VIWGKTPKFR
          =====
  
```

```

551 LPVQKEVWET WWSEYWQATW IPDWXVNTTP PLVKLWYQLE TEPIPGAETF
=====
601 YVDGAANRET KKGKAGYVTD RGRQKIVNLE NTTNQAELT AVYLALQDAE
=====
651 HIVNIVTDSQ YVLGIIHSQP DQSESELVNL IIEELIKKEK SYLSWVPAHK
=====
701 GVGGNEQVDK LVSSGNQKSS LFRWYRLSTR KNMRKYHNNW RAMASDFNIP
=====
751 HIVAKELVAR CDKCQLKGEA MHGQVDCSPG IWQLDCTHLE GKVILVAVHV
=====
801 ASGYLEAEVI PAETGQETAY FILKLAGRWP VKVIHTDNGP NFTSNTVKAA
=====
851 CWWAGIQQEF GIPYNPQSOG VVESMNKELK KIIGQIREQA EHLRTAVQMA
=====
901 VFIHNFKRKG GIGGYTAGER IIDIIATDIQ TTNLQKQILK VQNFRVYYRD
=====
951 SRDPIWKGPA RLLWKGEAV VIKEREEVKV IPRRKAKIIR DYGKQMAGDD
=====
1001 SMAGGQDESQ GLE
=====

```

HITS AT: 1-1013

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 51 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 256915-31-8 REGISTRY

CN Double-stranded RNA-binding protein (human clone NT1 gene STAU2) (9CI)
(CA INDEX NAME)

OTHER NAMES:

CN 1899: PN: WO0153312 SEQID: 2273 claimed sequence

CN Protein (human clone 784CIF2B_161 precursor)

FS PROTEIN SEQUENCE

SQL 479

PATENT ANNOTATIONS (PNTE):

Sequence |Patent

Source |Reference

=====+=====

Not Given|WO2001053312

|claimed

|SEQID 2273

```

SEQ      1 MLQINQMFSV QLSLGEQTWE SEGSSIKKAQ QAVANKALTE STLPKPVQKP
=====
      51 PKSNVNNNPG SITPTVELNG LAMKRGEPAI YRPLDPKPPF NYRANYNFRG
=====
     101 MYNQRYHCPV PKIFYVQLTV GNNEFFGEGK TRQAARHNAA MKALQALQNE
=====
     151 PIPERSPQNG ESGKMDDDDK DANKSEISLV FEIALKRNP VSFEVIKESG
=====
     201 PPHMKSFVTR VSVGEFSAEG EGNSKKLSKK RAATTVLQEL KKLPLPVVE
=====
     251 KPCLFFKKRP KTIVKAGPEY GQGMNPISRL AQIQQAKKEK EPDYVLLSER

```

```

=====
301 GMPRRREFVM QVKVGNEVAT GTGPNKKIAK KNAAEAMLLQ LGYKASTNLQ
=====
351 DQLEKTGENK GWSGPKPGFP EPTNNTPKGI LHLSPDVYQE MEASRHKVIS
=====
401 GTTLGYLSPK DMNQPSSSFF SISPTSNSA TIARELLMNG TSSTAEAIGL
=====
451 KGSSPTPPCS PVQPSKQLEY LARIQGFQV
=====

```

HITS AT: 1-479

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal; Patent

RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
 OCCU (Occurrence); PRP (Properties); USES (Uses)

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 52 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 247916-06-9 REGISTRY

CN Protein mAKAP (muscle A-kinase anchoring protein) (Rattus norvegicus
 strain Sprague-Dawley) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN GenBank AAD39150

CN GenBank AAD39150 (Translated from: GenBank AF139518)

CN Protein mAKAP (muscle A-kinase anchoring protein) (rat strain
 Sprague-Dawley)

FS PROTEIN SEQUENCE

SQL 2314

```

SEQ      1 MLTMSVTLSL LRSQGPDPMA TDASPMANM TPTVEQEEGE GEEAVKAIDA
=====
      51 EQQYGKPPPL HTAADWKIVL HLPEIETWLR MTSERVRDLT YSVQQDADSK
=====
     101 HVDVHLVQLK DICEDISDHV EQIHALLETE FSLKLLSYSV NVIVDIHAVQ
=====
     151 LLWHQLRVSV LVLRRERILQ LQDANGNYTR QTDILQAFSE ETTEGRDLSL
=====
     201 TEVDDSGQLT IKCSQDYLSL DCGITAFELS DYSPSEDLLG GLGDMTTSQA
=====
     251 KTKSFDWSY SEMEKEFPPEL IRSVGLLTVA TEPVPSSCGE ANEDSSQASL
=====
     301 SDDHKGEHGE DGAPVPGQQL DSTVGMSSLD GTLANAAEHP SETAKQDSTS
=====
     351 SPQLGAKKTQ PGPCEITTPK RSIRDCFNYN EDSPTQPTLP KRGLFLKETQ
=====
     401 KNERKGS DRK GQVVDLKPPEL SRSTPSLVDP PDRSKLCLVL QSSYPSSPSA
=====
     451 ASQSYECLHK VGLGNLENIV RSHIKEISS LGRLTDCHKE KLRLKKPHKT
=====
     501 LAEVSLCRIP KQGGGSGKRS ESTGSSAGPS MVSPGAPKAT MRPETDSAST
=====
     551 ASGGLCHQRN RSGQLPVQSK ASSSPPCSHS SESSLGSDSI KSPVPLLSKN
=====
     601 KSQKSSPPAP CHATQNGQVV EAWYGSDEYL ALPSHLKQTE VLALKLES LT

```



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=====
651 KLLPQKPRGE TIQDIDDWEL SEMNSDSEIY PTYHIKKKHT RLGTVSPSSS
=====
701 SDIASSLGES IESGPLSDIL SDEDLCLPLS SVKKFTDEKS ERPSSEKNE
=====
751 SHSATRSALI QKLMHDIQHQ ENYEAIWERI EGFVNKLDEF IQWLNEAMET
=====
801 TENWTPPKAE TDSLRLYLET HLSFKLNVD S HCALKEAVEE EGHQLLELVV
=====
851 SHKAGLKDTL RMIASQWKEL QRQIKRQHSW ILRALDTIKA EILATDVSVE
=====
901 DEEGTGSPKA EVQLCHLETQ RDAVEQMSLK LYSEQYTS GS KRKEEFANMS
=====
951 KAHAEGSNGL LDFDSEYQEL WDWLIDMESL VMDSHDLMMS EEQQQHLYKR
=====
1001 YSVEMSIRHL KKSELLSKVE ALKKGGLSLP DDILEKVDSI NEKWELLGKT
=====
1051 LREKIQDTIA GHSGSGPRDL LSPESGSLVR QLEVRIKELK RWLRDTELF I
=====
1101 FNSCLRQEKE GTSAEKQLQY FKSLCREIKQ RRRGVASILR LCQHLLDDRD
=====
1151 TCNLNADHQP MQLIIVNLER RWEAIVMQAV QWQTRLQKKM GKESETLNVI
=====
1201 DPGLMDLNGM SEDALEWDET DISNKLISVH EESNDLDQDP EPMLPAVKLE
=====
1251 ETHHKDSGYE EEAGDCGGSP YTSNITAPSS PHIYQVYSLH NVELHEDSHT
=====
1301 PFLKSSPKFT GTTQPTVLTK SLSKDSSFSS TKSLPDLLGG SGLVRPY SCH
=====
1351 SGDLSQNSGS ESGIVSEGDN EMPTNSDMSL FSMVDGSPSN PETEHPDPQM
=====
1401 GDAANVLEQK FKDNGESIKL SSVSRASVSP VGCVNGKAGD LNSVTKHTAD
=====
1451 CLGEELQGKH DVFTFYDYSY LQGSKLKLP IMKQPQSEKA HVEDPLLGGF
=====
1501 YFDKKCKAK HQASESQPDA PPHERILASA PHEMGRSAYK SSDIEKTFTG
=====
1551 IQSARQLSLL SRSSSVESLS PGDDLFG LGI FKNGSDSLQR STSLESWLTS
=====
1601 YKSNEDLFSC HSSGDISVSS GSVGELSKRT LDLLNRLENI QSPSEQIKR
=====
1651 SVSDMTLQSS SQKMPFAGQM SLDVASSINE DSPASLTELS SDELSLCSE
=====
1701 DIVLHKNKIP ESNASFRKRL NRSVAESDV NVSMIVNVSC TSACTDDEDD
=====
1751 SDLLSSSTLT LTEEELCLKD EDDSSSIATD DEIYEESNLM SGLDYIKNEL
=====
1801 QTWIRPKLSL TREKKRSGVT DEIKVNKDGG GNEKANPSDT LDIEALLNGS
=====
1851 IRCLSENNGN GKTPPRTHGS GTKGENKKST YDVSKDPHVA DMENGNIEST
=====
1901 PEREREKPQG LPEVSENLAS NVKTISESEL SEYEAVMDGS EDSSVARKEF
=====
1951 CPPNDRHPPQ MGPKLQHPEN QSGDCKPVQN PCPGLLSEAG VGSRQDSNGL
=====
2001 KSLPNDAPSG ARKPAGCCLL EQNETEESAS ISSNASCCNC KPDV FHQKDD
=====
2051 EDCSVHDFVK EIIDMASTAL KSKSQPESEV AAPTSLTQIK EKVLEHSHRP
=====
2101 IHLRKGDFYS YLSLSSHDS D CGEVTNYIDE KSSTPLPPDA VDSGLDDKED
=====

```

```

=====
2151 MDCFFEACVE DEPVNEEAGL PGALPNESAI EDGAEQKSEQ KTASSPVLSD
=====
2201 KTDLVPLSGL SPQKGADDAK EGDDVSHTSQ GCAESTEPTT PSGKANAEGR
=====
2251 SRMQGVSATP EENAASAKPK IQAFSLNAKQ PKGKVAMRYP SPQTLTCKEK
=====
2301 LVNFHEDRHS NMHR
=====

```

HITS AT: 1-2314

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);
PROC (Process); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 53 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 211809-45-9 REGISTRY

CN Docking protein DP (human gene HsPex14p peroxisome-associated) (9CI) (CA
INDEX NAME)

OTHER NAMES:

CN Peroxin (Cricetulus longicaudatus CHO-K1 gene Pex14)

CN Peroxisomal membrane anchor protein (Cricetulus longicaudatus CHO-K1 gene
Pex14)

FS PROTEIN SEQUENCE

SQL 377

```

SEQ      1 MASSEQAEQP SQPSSTPGSE NVLPREPLIA TAVKFLQNSR VRQSPLATRR
=====
      51 AFLKKKGLTD EEIDMAFQQS GTAADPSSL GPATQVVPVQ PPHLISQPYS
=====
     101 PAGSRWRDYG ALAIIMAGIA FGFHQLYKKY LLPLILGGRE DRKQLERMEA
=====
     151 GLSELSGSAV QTVTQLQTTL ASVQELLIQQ QQKIQELAHE LAAAKATTST
=====
     201 NWILESQNIN ELKSEINSLK GLLNRRQFP PSPSAPKIPS WQIPVKSPSP
=====
     251 SSPAAVNHHS SSDISPVSNE STSSSPGKEG HSPEGSTVTY HLLGPQEEGE
=====
     301 GVV DVKGQVR MEVQGEEEKR EDKEDEEDEE DDDVSHVDEE DCLGVQREDR
=====
     351 RGGDGQINEQ VEKLRRPEGA SNESERD
=====

```

HITS AT: 1-377

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)
2 REFERENCES IN FILE CA (1907 TO DATE)

2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 54 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 209277-31-6 REGISTRY
 CN Kinase (phosphorylating), gene flrB protein (Vibrio cholerae strain 0395)
 (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN Sensory box sensor histidine kinase (Vibrio cholerae strain N16961 gene
 VC2136)
 FS PROTEIN SEQUENCE
 SQL 351

```

SEQ      1 MMSSAVQEQH SHLDSLEDQV ERYKQVLDVM PAGVILLDTQ GIVREANPEA
          =====
        51 QRLLDVPLVG EKWYSVIQIA FAPRDDDGE ISLRNGRKVR LAISASTTQ
          =====
       101 LILITDLTET RLLQSRISDL QRLSSLGRMV ASLAHQVRTP LSSAMLYAAN
          =====
       151 LAAPNLPPAT RERFQSKLVD RLHDLEKQVN DMLLFAKGGD NKVVMPSIG
          =====
       201 DLAAEFMPMV ETALKNNQID YGQEVSEET MLLGNANALA SALSNLVMNA
          =====
       251 LQIAGKGSQI DVFFRPVNGE LKISVQDNGP GVPESLQHKI MEPFFTTRSQ
          =====
       301 GTGLGLAVVQ MVCRAHGGRL ELISKEGEGA CFTMCIPLER QADSSNSETG
          =====
       351 E
          =

```

HITS AT: 1-351

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified
 CI MAN
 SR CA
 LC STN Files: CA, CAPLUS, TOXCENTER
 DT.CA Caplus document type: Journal
 RL.NP Roles from non-patents: BIOL (Biological study); PROC (Process); PRP
 (Properties)
 2 REFERENCES IN FILE CA (1907 TO DATE)
 2 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 55 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN
 RN 179310-03-3 REGISTRY
 CN Phosphatase, phosphoprotein (phosphotyrosine) (human clone hPtPκ
 isoenzyme κ) (9CI) (CA INDEX NAME)
 OTHER NAMES:
 CN GenBank CAA94519
 CN GenBank CAA94519 (Translated from: GenBank Z70660)
 FS PROTEIN SEQUENCE
 SQL 1439

```

SEQ      1 MDTTAAAALP AFVALLLLSP WPLLGSAQGQ FSAGGCTFDD GPGACDYHQD
          =====
        51 LYDDFEWVHV SAQEPHYLPP EMPQGSYMIV DSSDHDPGEK ARLQLPTMKE
          =====
       101 NDTHCIDFSY LLYSQKGLNP GTLNILVRVN KGPLANPIWN VTGFTGRDWL
          =====
       151 RAELAVSSFW PNEYQVIFEA EVSGGRSGYI AIDDIQVLSY PCDKSPHFLR
          =====
       201 LGDVEVNAGQ NATFQCIATG RDAVHNKLWL QRRNGEDIPV AQTKNINHRR
          =====
       251 FAASFRLQEV TKTDQDLYRC VTQSERGSGV SNFAQLIVRE PPRPIAPPQL
          =====

```

```

301 LGVGPTYLLI QLNANSIIGD GPIILKEVEY RMTSGSWTET HAVNAPTYKL
=====
351 WHLDPDTEYE IRVLLTRPGE GGTGLPGPPL ITRTKCAEPM RTPKTLKIAE
=====
401 IQARRIAVDW ESLGYNITRC HTFNVTCYH YFRGHNESKA DCLDMDPKAP
=====
451 QHVVNHLPPY TNVSLKMILT NPEGRKESEE TIIQTDEDVP GPVPVKSLQG
=====
501 TSFENKIFLN WKEPLDPNGI ITQYEISYSS IRSFDPAPVP AGPPQTVSNL
=====
551 WNSTHHVFMH LHPGTTYQFF IRASTVKGFG PATAINVTN ISAPTLPDYE
=====
601 GVDASLNETA TTITVLLRPA QAKGAPISAY QIVVEELHPH RTKREAGAME
=====
651 CYQVPVTTYQN AMSSGAPYYF AAELPPGNLP EPAPFTVGDN RTYQGFWNPP
=====
701 LAPRKGYNII FQAMSSVEKE TKTQCVRIAT KAATEEPEVI PDKAQTDREV
=====
751 VKIAGISAGI LVFILLLLVV ILIVKKSCLA KKRKDAMGNT RQEMTHMVNA
=====
801 MDRSYADQST LHAEDPLSIT FMDQHNFSPR YENHSATAES SRLLDVPRYL
=====
851 CEGTESPYQT GQLHPAIRVA DLLQHINLMK TSDSYGFKEE YESFFEGQSA
=====
901 SWDVAKKDQN RAKNRYGNII AYDHSRVILQ PVEDDPSSDY INANYIDGYQ
=====
951 RPSHYIATQG PVHETVYDFW RMIWQEQSAC IVMVTNLVEV GRVKCYKYWP
=====
1001 DDTEVYGDFK VTCVEMEPLA EYVVRTFTLE RRGYNEIREV KQFHFTGWPD
=====
1051 HGVPYHATGL LSFIRRVKLS NPPSAGPIVV HCSAGAGRTG CYIVIDIMLD
=====
1101 MAEREGVVDI YNCVKALRSR RINMVQTEEQ YIFIHDAILE ACLCGETAIP
=====
1151 VCEFKAAYFD MIRIDSQTNS SHLKDEFQTL NSVTPRLQAE DCSIACLPRN
=====
1201 HDKNRFDML PPDRCLPFLI TIDGESSNYI NAALMDSYRQ PAAFIVTQYP
=====
1251 LPNTVKDFWR LVYDYGCTSI VMLNEVDLSQ GCPQYWPEEG MLRYGPIQVE
=====
1301 CMSCSMDCDV INRIFRICNL TRPQEGYLMV QQFQYLGWAS HREVPKSKRS
=====
1351 FLKLILQVEK WQEECEELEG RTIIHCLNGG GRSGMFCAIG IVVEMVKRQN
=====
1401 VVDVFHAVKT LRNSKPNMVE APEQYRFCYD VALEYLESS
=====

```

HITS AT: 1-1439

****RELATED SEQUENCES AVAILABLE WITH SEQLINK****

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);
PROC (Process); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 56 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 174597-29-6 REGISTRY
 CN Protein (Thermus aquaticus strain YT1 gene mutS DNA mismatch repair) (9CI)
 (CA INDEX NAME)
 OTHER NAMES:
 CN Phosphatase, adenosine tri- (Thermus aquaticus strain YT1 gene mutS)
 FS PROTEIN SEQUENCE
 SQL 811

```

SEQ      1 MEGMLKGEGP GPLPPLLQOY VELRDQYPDY LLLFQVGDFY ECFGEDAERL
          =====
      51 ARALGLVLTH KTSKDFTTPM AGIPLRAFEA YAERLLKMGF RLAVADQVEP
          =====
     101 AEEAEGLVRR EVTQLLTPGT LLQESLLPRE ANYLAAIATG DGWGLAFLDV
          =====
     151 STGEFKGTVL KSKSALYDEL FRHRPAEVLL APELLENGAF LDEFKRFRFPV
          =====
     201 MLSEAPFEPE GEGPLALRRA RGALLAYAQR TQGGALSLOP FRFYDPGAFM
          =====
     251 RLPEATLRAL EVFEPLRGQD TLFVSVLDETR TAPGRRLLOQ WLRHPLLDGR
          =====
     301 PLEARLDREVE GFVREGALRE GVRRLLYRLA DLERLATRLE LGRASPKDLG
          =====
     351 ALRRSLQILP ELRALLGEEV GLPDLSPKE ELEAALVEDP PLKVSEGGI
          =====
     401 REGYDPDLDA LRAAHREGVA YFLELEERER ERTGIPTLKV GYNAVFGYYL
          =====
     451 EVTRPYPERV PKEYRPVQTL KDRQRYTLPE MKEKEREVYR LEALIRRREE
          =====
     501 EVFLEVRERA KRQAEALREA ARILAELDVY AALAEVAVRY GYVRPRFGDR
          =====
     551 LQIRAGRHPV VERRTEFVPN DLEMAHELVL ITGPNMAGKS TFLRQTALIA
          =====
     601 LLAQVGSFVP AEEAHLPLFD GIYTRIGASD DLAGGKSTFM VEMEEVALIL
          =====
     651 KEATENSLVL LDEVGRGTSS LDGVAIATAV AEALHERRAY TLFATHYFEL
          =====
     701 TALGLPRLKN LHVAAREEAG GLVIFYHQVLP GPASKSYGVE VAAMAGLPKE
          =====
     751 VVARARALLQ AMAARREGAL DAVLERLLAL DPDRLTPLA LRLQLKAL
          =====
     801 ALGAPLDTMK G
          =====
  
```

HITS AT: 1-811

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); OCCU (Occurrence);
 PREP (Preparation); PROC (Process); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 57 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 161631-10-3 REGISTRY

CN Phosphatase, adenosine tri- (Helicobacter pylori clone pBHpC8 gene copA)
 (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Phosphatase, adenosine tri- (Campylobacter pyloridis clone pBHpC8 gene
copA)
FS PROTEIN SEQUENCE
SQL 611

```

SEQ      1 MHWGRDFYIQ GFKALWHRQP NMSSLIAIGT SAALISLWQ LYLVTYDHYT
          =====
          51 DQWSYGHYYF ESVCVILMFV MVGKRIENV S KDKALDAMQA LMKNAPKTAL
          =====
          101 KIQNDQQIEV LVDSIVVGDI LKVLPGTLIA VDGEIIEGEG ELDESMLSGE
          =====
          151 ALPVYKKVGD KVFSGTFNSH TSFLMKATQN NKNSTLSQIV EMIHNAQSSK
          =====
          201 AEISRLADKV SSVFVPSVIA IAILAFVWL IIAPKPDFWW NFGIALEV FV
          =====
          251 SVLVISCPCSC FRIGYAMSIL VANQKSEFFR IIFKDAKSLE KARLVNTIVF
          =====
          301 DKTGTLTNGK PVVKS VHSKI ELLELLSLAN SIEKSSEHVI AKGIVEYAKE
          =====
          351 HNAPLKEMSE VKVKTGFGIS AKTDYQGTKE IIKVGNSEFF NPINTLEIQE
          =====
          401 NGNFSLVGRA INEKEDELLG AFVLEDLPKK GVKEHVAQIK NLGINTFLLS
          =====
          451 GDNRENVKKC ALELGIDGYI SNAKPQDKLN KIKELKEKGR IVMMVGDGLN
          =====
          501 DAPSLAMSDV AVVMAKGSDV SVQAADIVSF NNDIKSVYSA IKLSQATIKN
          =====
          551 IKENLFWAFC YNSVFIPLAC GVLYKANIML SPAIAGLAMS LSSVSVVLNS
          =====
          601 QRLRNFKIKD H
          =====

```

HITS AT: 1-611

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, TOXCENTER

DT.CA CAplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

1 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

L50 ANSWER 58 OF 58 REGISTRY COPYRIGHT 2005 ACS on STN

RN 148500-01-0 REGISTRY

CN Protein (human gene RING1 reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Gene RING1 protein (human)

CN Protein (human clone Y42 gene RING1 ring-finger)

CN Ring finger protein 1 (human clone 1033B10 gene dJ1033B10.6)

FS PROTEIN SEQUENCE

SQL 377

```

SEQ      1 MDGTEIAVSP RSLHSELMCP ICLDMLKNTM TTKECLHRFC SDCIVTALRS
          =====
          51 GNKECPTCRK KLVSKRSLRP DPNFDALISK IYPSREEYEA HQDRV LIRLS
          =====
          101 RLHNQQALSS SIEEGLRMQA MHRAQVRVRP IPGSDQTTM SGGE GEPGEG
          =====
          151 EGDGEDVSSD SAPDSAPGPA PKRPRGGGAG GSSVGTGGGG TGGVGGGAGS
          =====
          201 EDSGDRGGTL GGGTLGPPSP PGAPSPPEPG GEIELVFRPH PLLVEKGEYC

```

```

=====
251 QTRYVKTTGN ATVDHLSKYL ALRIALERRQ QQEAGEPGGP GGGASDTGGP
=====
301 DCGGEGEGGA GGGDGPEEPA LPSLEGVSEK QYTIYIAPGG GAFTTLNGSL
=====
351 TLELVNEKFW KVSRLPLELCY APTKDPK
=====

```

HITS AT: 1-377

RELATED SEQUENCES AVAILABLE WITH SEQLINK

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS

DT.CA Caplus document type: Journal

RL.NP Roles from non-patents: BIOL (Biological study); PRP (Properties)

3 REFERENCES IN FILE CA (1907 TO DATE)

3 REFERENCES IN FILE CAPLUS (1907 TO DATE)

Rooke 10/015,956

=> d cost

COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
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NETWORK CHARGES	0.06	13.50
SEARCH CHARGES	0.00	229.20
DISPLAY CHARGES	0.00	435.82
OTHER CHARGES	0.00	10.50
	-----	-----
FULL ESTIMATED COST	2.45	1044.75

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)

	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-9.49

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=>